

配 列 表

SEQUENCING LISTING

<110> KYOWA HAKKO KOGYO CO., LTD

<111> THE CELL HAVING THE POTENTIALITY OF DIFFERENTIATION INTO
CARDIOMYOCYTES

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<150> H11-372826

<151> 1999-12-28

<150> PCT-JP00-01148

<151> 2000-02-28

<150> PCT-JP00-07741

<151> 2000-11-02

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<170> PatentIn Ver.2.0

<210> 1

<211> 411

<212> PRT

<213> Homo sapiens

<400> 1

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Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile

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Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly

35

40

45

Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
 50 55 60
 Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
 65 70 75 80
 Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
 85 90 95
 Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
 100 105 110
 Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
 115 120 125
 Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
 130 135 140
 Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
 145 150 155 160
 Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
 165 170 175
 Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
 180 185 190
 Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
 195 200 205
 Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
 210 215 220
 Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
 225 230 235 240
 Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
 245 250 255
 Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
 260 265 270
 Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
 275 280 285
 Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
 290 295 300
 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
 305 310 315 320
 Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
 325 330 335

Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
 340 345 350
 Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
 355 360 365
 Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
 370 375 380
 Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
 385 390 395 400
 Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
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<210> 2

<211> 1233

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1236)

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 Gly Glu Ser Ala Ala Gly Gly Ser Gly Ala Gly Gly Asp Ser Ala Ile
 20 25 30
 gag cag ggg ggc cag ggc agc gcg ctc gcc ccg tcc ccg gtg agc ggc 144
 Glu Gln Gly Gly Gln Gly Ser Ala Leu Ala Pro Ser Pro Val Ser Gly
 35 40 45
 gtg cgc agg gaa ggc gct cgg ggc ggc ggc cgt ggc cgg ggg cgg tgg 192
 Val Arg Arg Glu Gly Ala Arg Gly Gly Gly Arg Gly Arg Gly Arg Trp
 50 55 60
 aag cag gcg ggc cgg ggc ggc ggc gtc tgt ggc cgt ggc cgg ggc cgg 240
 Lys Gln Ala Gly Arg Gly Gly Gly Val Cys Gly Arg Gly Arg Gly Arg
 65 70 75 80
 ggc cgt ggc cgg gga cgg gga cgg ggc cgg ggc cgg ggc cgc ggc cgt 288
 Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
 85 90 95

ccc ccg agt ggc ggc agc ggc ctt ggc ggc gac ggc ggc ggc tgc ggc 336
 Pro Pro Ser Gly Gly Ser Gly Leu Gly Gly Asp Gly Gly Gly Cys Gly
 100 105 110
 ggc ggc ggc agc ggt ggc ggc ggc gcc ccc cgg cgg gag ccg gtc cct 384
 Gly Gly Gly Ser Gly Gly Gly Gly Ala Pro Arg Arg Glu Pro Val Pro
 115 120 125
 ttc ccg tcg ggg agc gcg ggg ccg ggg ccc agg gga ccc cgg gcc acg 432
 Phe Pro Ser Gly Ser Ala Gly Pro Gly Pro Arg Gly Pro Arg Ala Thr
 130 135 140
 gag agc ggg aag agg atg gat tgc ccg gcc ctc ccc ccc gga tgg aag 480
 Glu Ser Gly Lys Arg Met Asp Cys Pro Ala Leu Pro Pro Gly Trp Lys
 145 150 155 160
 aag gag gaa gtg atc cga aaa tct ggg cta agt gct ggc aag agc gat 528
 Lys Glu Glu Val Ile Arg Lys Ser Gly Leu Ser Ala Gly Lys Ser Asp
 165 170 175
 gtc tac tac ttc agt cca agt ggt aag aag ttc aga agc aag cct cag 576
 Val Tyr Tyr Phe Ser Pro Ser Gly Lys Lys Phe Arg Ser Lys Pro Gln
 180 185 190
 ttg gca agg tac ctg gga aat act gtt gat ctc agc agt ttt gac ttc 624
 Leu Ala Arg Tyr Leu Gly Asn Thr Val Asp Leu Ser Ser Phe Asp Phe
 195 200 205
 aga act gga aag atg atg cct agt aaa tta cag aag aac aaa cag aga 672
 Arg Thr Gly Lys Met Met Pro Ser Lys Leu Gln Lys Asn Lys Gln Arg
 210 215 220
 ctg cga aac gat cct ctc aat caa aat aag ggt aaa cca gac ttg aat 720
 Leu Arg Asn Asp Pro Leu Asn Gln Asn Lys Gly Lys Pro Asp Leu Asn
 225 230 235 240
 aca aca ttg cca att aga caa aca gca tca att ttc aaa caa ccg gta 768
 Thr Thr Leu Pro Ile Arg Gln Thr Ala Ser Ile Phe Lys Gln Pro Val
 245 250 255
 acc aaa gtc aca aat cat cct agt aat aaa gtg aaa tca gac cca caa 816
 Thr Lys Val Thr Asn His Pro Ser Asn Lys Val Lys Ser Asp Pro Gln
 260 265 270
 cga atg aat gaa cag cca cgt cag ctt ttc tgg gag aag agg cta caa 864
 Arg Met Asn Glu Gln Pro Arg Gln Leu Phe Trp Glu Lys Arg Leu Gln
 275 280 285

gga ctt agt gca tca gat gta aca gaa caa att ata aaa acc atg gaa 912
 Gly Leu Ser Ala Ser Asp Val Thr Glu Gln Ile Ile Lys Thr Met Glu
 290 295 300
 cta ccc aaa ggt ctt caa gga gtt ggt cca ggt agc aat gat gag acc 960
 Leu Pro Lys Gly Leu Gln Gly Val Gly Pro Gly Ser Asn Asp Glu Thr
 305 310 315 320
 ctt tta tct gct gtt gcc agt gct ttg cac aca agc tct gcg cca atc 1008
 Leu Leu Ser Ala Val Ala Ser Ala Leu His Thr Ser Ser Ala Pro Ile
 325 330 335
 aca ggg caa gtc tcc gct gct gtg gaa aag aac cct gct gtt tgg ctt 1056
 Thr Gly Gln Val Ser Ala Ala Val Glu Lys Asn Pro Ala Val Trp Leu
 340 345 350
 aac aca tct caa ccc ctc tgc aaa gct ttt att gtc aca gat gaa gac 1104
 Asn Thr Ser Gln Pro Leu Cys Lys Ala Phe Ile Val Thr Asp Glu Asp
 355 360 365
 atc agg aaa cag gaa gag cga gta cag caa gta cgc aag aaa ttg gaa 1152
 Ile Arg Lys Gln Glu Glu Arg Val Gln Gln Val Arg Lys Lys Leu Glu
 370 375 380
 gaa gca ctg atg gca gac atc ttg tgc cga gct gct gat aca gaa gag 1200
 Glu Ala Leu Met Ala Asp Ile Leu Ser Arg Ala Ala Asp Thr Glu Glu
 385 390 395 400
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 Met Asp Ile Glu Met Asp Ser Gly Asp Glu Ala
 405 410

<210> 3

<211> 196

<212> PRT

<213> Homo sapiens

<400> 3

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 His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg
 20 25 30
 Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu
 35 40 45
 Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg

50	55	60
Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu		
65	70	75
Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys		
85	90	95
Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro		
100	105	110
Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg		
115	120	125
Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg		
130	135	140
Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys		
145	150	155
Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu		
165	170	175
Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp		
180	185	190
Thr Asp Val Arg		
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<210> 4

<211> 588

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(591)

<400> 4

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cat gtt ctg gcc gag gaa gcc gag atc ccc cgc gag gtg atc gag agg	96
His Val Leu Ala Glu Glu Ala Glu Ile Pro Arg Glu Val Ile Glu Arg	
20 25 30	
ctg gcc cgc agt cag atc cac agc atc cgg gac ctc cag cga ctc ctg	144
Leu Ala Arg Ser Gln Ile His Ser Ile Arg Asp Leu Gln Arg Leu Leu	
35 40 45	

gag ata gac tcc gta ggg agt gag gat tct ttg gac acc agc ctg aga 192
 Glu Ile Asp Ser Val Gly Ser Glu Asp Ser Leu Asp Thr Ser Leu Arg
 50 55 60
 gct cac ggg gtc cac gcc act aag cat gtg ccc gag aag cgg ccc ctg 240
 Ala His Gly Val His Ala Thr Lys His Val Pro Glu Lys Arg Pro Leu
 65 70 75 80
 ccc att cgg agg aag aga agc atc gag gaa gct gtc ccc gct gtc tgc 288
 Pro Ile Arg Arg Lys Arg Ser Ile Glu Glu Ala Val Pro Ala Val Cys
 85 90 95
 aag acc agg acg gtc att tac gag att cct cgg agt cag gtc gac ccc 336
 Lys Thr Arg Thr Val Ile Tyr Glu Ile Pro Arg Ser Gln Val Asp Pro
 100 105 110
 acg tcc gcc aac ttc ctg atc tgg ccc ccg tgc gtg gag gtg aaa cgc 384
 Thr Ser Ala Asn Phe Leu Ile Trp Pro Pro Cys Val Glu Val Lys Arg
 115 120 125
 tgc acc ggc tgc tgc aac acg agc agt gtc aag tgc cag ccc tcc cgc 432
 Cys Thr Gly Cys Cys Asn Thr Ser Ser Val Lys Cys Gln Pro Ser Arg
 130 135 140
 gtc cac cac cgc agc gtc aag gtg gcc aag gtg gaa tac gtc agg aag 480
 Val His His Arg Ser Val Lys Val Ala Lys Val Glu Tyr Val Arg Lys
 145 150 155 160
 aag cca aaa tta aaa gaa gtc cag gtg agg tta gag gag cat ttg gag 528
 Lys Pro Lys Leu Lys Glu Val Gln Val Arg Leu Glu Glu His Leu Glu
 165 170 175
 tgc gcc tgc gcg acc aca agc ctg aat ccg gat tat cgg gaa gag gac 576
 Cys Ala Cys Ala Thr Thr Ser Leu Asn Pro Asp Tyr Arg Glu Glu Asp
 180 185 190
 acg gat gtg agg 588
 Thr Asp Val Arg
 195

<210> 5

<211> 241

<212> PRT

<213> Homo sapiens

<400> 5

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Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu			
35	40	45	
His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met			
50	55	60	
Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg			
65	70	75	80
Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu			
85	90	95	
Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp			
100	105	110	
Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln			
115	120	125	
Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr			
130	135	140	
Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg			
145	150	155	160
Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu			
165	170	175	
Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser			
180	185	190	
Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val			
195	200	205	
Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg			
210	215	220	
Lys Phe Lys His Thr His Asp Lys Thr Ala Leu Lys Glu Thr Leu Gly			
225	230	235	240

Ala

<210> 6

<211> 723

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(726)

<400> 6

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ctg gtc agc gcc gag ggg gac ccc att ccc gag gag ctt tat gag atg	96
Leu Val Ser Ala Glu Gly Asp Pro Ile Pro Glu Glu Leu Tyr Glu Met	
20 25 30	
ctg agt gac cac tgc atc cgc tcc ttt gat gat etc caa cgc ctg ctg	144
Leu Ser Asp His Ser Ile Arg Ser Phe Asp Asp Leu Gln Arg Leu Leu	
35 40 45	
cac gga gac ccc gga gag gaa gat ggg gcc gag ttg gac ctg aac atg	192
His Gly Asp Pro Gly Glu Glu Asp Gly Ala Glu Leu Asp Leu Asn Met	
50 55 60	
acc cgc tcc cac tct gga ggc gag ctg gag agc ttg gct cgt gga aga	240
Thr Arg Ser His Ser Gly Gly Glu Leu Glu Ser Leu Ala Arg Gly Arg	
65 70 75 80	
agg agc ctg ggt tcc ctg acc att gct gag ccg gcc atg atc gcc gag	288
Arg Ser Leu Gly Ser Leu Thr Ile Ala Glu Pro Ala Met Ile Ala Glu	
85 90 95	
tgc aag acg cgc acc gag gtg ttc gag atc tcc cgg cgc etc ata gac	336
Cys Lys Thr Arg Thr Glu Val Phe Glu Ile Ser Arg Arg Leu Ile Asp	
100 105 110	
cgc acc aac gcc aac ttc ctg gtg tgg ccg ccc tgt gtg gag gtg cag	384
Arg Thr Asn Ala Asn Phe Leu Val Trp Pro Pro Cys Val Glu Val Gln	
115 120 125	
cgc tgc tcc ggc tgc tgc aac aac cgc aac gtg cag tgc cgc ccc acc	432
Arg Cys Ser Gly Cys Cys Asn Asn Arg Asn Val Gln Cys Arg Pro Thr	
130 135 140	
cag gtg cag ctg cga cct gtc cag gtg aga aag atc gag att gtg cgg	480
Gln Val Gln Leu Arg Pro Val Gln Val Arg Lys Ile Glu Ile Val Arg	
145 150 155 160	
aag aag cca atc ttt aag aag gcc acg gtg acg ctg gaa gac cac ctg	528
Lys Lys Pro Ile Phe Lys Lys Ala Thr Val Thr Leu Glu Asp His Leu	
165 170 175	
gca tgc aag tgt gag aca gtg gca gct gca cgg cct gtg acc cga agc	576

Ala Cys Lys Cys Glu Thr Val Ala Ala Ala Arg Pro Val Thr Arg Ser
 180 185 190
 ccg ggg ggt tcc cag gag cag cga gcc aaa acg ccc caa act cgg gtg 624
 Pro Gly Gly Ser Gln Glu Gln Arg Ala Lys Thr Pro Gln Thr Arg Val
 195 200 205
 acc att cgg acg gtg cga gtc cgc cgg ccc ccc aag ggc aag cac cgg 672
 Thr Ile Arg Thr Val Arg Val Arg Arg Pro Pro Lys Gly Lys His Arg
 210 215 220
 aaa ttc aag cac acg cat gac aag acg gca ctg aag gag acc ctt gga 720
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 225 230 235 240
 gcc 723
 Ala
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 20 25 30
 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
 35 40 45
 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
 50 55 60
 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
 65 70 75 80
 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
 85 90 95
 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
 100 105 110
 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
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 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
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Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser

145

150

<210> 8

<211> 465

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(468)

<400> 8

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ggc agc ggc gcc ttc ccg ccc ggc cac ttc aag gac ccc aag cgg ctg	96
Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu	
20 25 30	
tac tgc aaa aac ggg ggc ttc ttc ctg cgc atc cac ccc gac ggc cga	144
Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg	
35 40 45	
gtt gac ggg gtc cgg gag aag agc gac cct cac atc aag cta caa ctt	192
Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu	
50 55 60	
caa gca gaa gag aga gga gtt gtg tct atc aaa gga gtg tgt gct aac	240
Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn	
65 70 75 80	
cgt tac ctg gct atg aag gaa gat gga aga tta ctg gct tct aaa tgt	288
Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys	
85 90 95	
gtt acg gat gag tgt ttc ttt ttt gaa cga ttg gaa tct aat aac tac	336
Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr	
100 105 110	
aat act tac cgg tca agg aaa tac acc agt tgg tat gtg gca ttg aaa	384
Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys	
115 120 125	
cga act ggg cag tat aaa ctt gga tcc aaa aca gga cct ggg cag aaa	432
Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys	

130 135 140
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 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
 145 150 155
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 <211> 324
 <212> PRT
 <213> Homo sapiens
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 20 25 30
 Leu Ser Ala Arg Leu Glu Ala Thr Leu Ala Pro Ser Ser Cys Met Leu
 35 40 45
 Ala Ala Phe Lys Pro Glu Ala Tyr Ala Gly Pro Glu Ala Ala Ala Pro
 50 55 60
 Gly Leu Pro Glu Leu Arg Ala Glu Leu Gly Arg Ala Pro Ser Pro Ala
 65 70 75 80
 Lys Cys Ala Ser Ala Phe Pro Ala Ala Pro Ala Phe Tyr Pro Arg Ala
 85 90 95
 Tyr Ser Asp Pro Asp Pro Ala Lys Asp Pro Arg Ala Glu Lys Lys Glu
 100 105 110
 Leu Cys Ala Leu Gln Lys Ala Val Glu Leu Glu Lys Thr Glu Ala Asp
 115 120 125
 Asn Ala Glu Arg Pro Arg Ala Arg Arg Arg Arg Lys Pro Arg Val Leu
 130 135 140
 Phe Ser Gln Ala Gln Val Tyr Glu Leu Glu Arg Arg Phe Lys Gln Gln
 145 150 155 160
 Arg Tyr Leu Ser Ala Pro Glu Arg Asp Gln Leu Ala Ser Val Leu Lys
 165 170 175
 Leu Thr Ser Thr Gln Val Lys Ile Trp Phe Gln Asn Arg Arg Tyr Lys
 180 185 190
 Cys Lys Arg Gln Arg Gln Asp Gln Thr Leu Glu Leu Val Gly Leu Pro
 195 200 205
 Pro Pro Pro Pro Pro Pro Ala Arg Arg Ile Ala Val Pro Val Leu Val

210	215	220
Arg Asp Gly Lys Pro Cys Leu Gly Asp Ser Ala Pro Tyr Ala Pro Ala		
225	230	235 240
Tyr Gly Val Gly Leu Asn Pro Tyr Gly Tyr Asn Ala Tyr Pro Ala Tyr		
245	250	255
Pro Gly Tyr Gly Gly Ala Ala Cys Ser Pro Gly Tyr Ser Cys Thr Ala		
260	265	270
Ala Tyr Pro Ala Gly Pro Ser Pro Ala Gln Pro Ala Thr Ala Ala Ala		
275	280	285
Asn Asn Asn Phe Val Asn Phe Gly Val Gly Asp Leu Asn Ala Val Gln		
290	295	300
Ser Pro Gly Ile Pro Gln Ser Asn Ser Gly Val Ser Thr Leu His Gly		
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Ile Arg Ala Trp		

<210> 10

<211> 972

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(975)

<400> 10

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Met Phe Pro Ser Pro Ala Leu Thr Pro Thr Pro Phe Ser Val Lys Asp	
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atc cta aac ctg gaa cag cag cag cgc agc ctg gct gcc gcc gga gag	96
Ile Leu Asn Leu Glu Gln Gln Gln Arg Ser Leu Ala Ala Ala Gly Glu	
20 25 30	
ctc tct gcc cgc ctg gag gcg acc ctg gcg ccc tcc tcc tgc atg ctg	144
Leu Ser Ala Arg Leu Glu Ala Thr Leu Ala Pro Ser Ser Cys Met Leu	
35 40 45	
gcc gcc ttc aag cca gag gcc tac gct ggg ccc gag gcg gct gcg ccg	192
Ala Ala Phe Lys Pro Glu Ala Tyr Ala Gly Pro Glu Ala Ala Ala Pro	
50 55 60	
ggc ctc cca gag ctg cgc gca gag ctg ggc cgc gcg cct tca ccg gcc	240

14/90

Pro Gly Tyr Gly Gly Ala Ala Cys Ser Pro Gly Tyr Ser Cys Thr Ala
 260 265 270
 get tac ccc gcc ggg cct tcc cca gcg cag ccg gcc act gcc gcc gcc 864
 Ala Tyr Pro Ala Gly Pro Ser Pro Ala Gln Pro Ala Thr Ala Ala Ala
 275 280 285
 aac aac aac ttc gtg aac ttc ggc gtc ggg gac ttg aat gcg gtt cag 912
 Asn Asn Asn Phe Val Asn Phe Gly Val Gly Asp Leu Asn Ala Val Gln
 290 295 300
 agc ccc ggg att ccg cag agc aac tcg gga gtg tcc acg ctg cat ggt 960
 Ser Pro Gly Ile Pro Gln Ser Asn Ser Gly Val Ser Thr Leu His Gly
 305 310 315 320
 atc cga gcc tgg 972
 Ile Arg Ala Trp
 324

<210> 11

<211> 442

<212> PRT

<213> Homo sapiens

<400> 11

Met Tyr Gln Ser Leu Ala Met Ala Ala Asn His Gly Pro Pro Pro Gly
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 20 25 30
 Ala Ser Ser Pro Val Tyr Leu Pro Thr Pro Arg Val Pro Ser Ser Val
 35 40 45
 Leu Gly Leu Ser Tyr Leu Gln Gly Gly Gly Ala Gly Ser Ala Ser Gly
 50 55 60
 Gly Pro Ser Gly Gly Ser Pro Gly Gly Ala Ala Ser Gly Ala Gly Pro
 65 70 75 80
 Gly Thr Gln Gln Gly Ser Pro Gly Trp Ser Gln Ala Gly Ala Thr Gly
 85 90 95
 Ala Ala Tyr Thr Pro Pro Pro Val Ser Pro Arg Phe Ser Phe Pro Gly
 100 105 110
 Thr Thr Gly Ser Leu Ala Ala Ala Ala Ala Ala Ala Ala Arg Glu
 115 120 125
 Ala Ala Ala Tyr Ser Ser Gly Gly Gly Ala Ala Gly Ala Gly Leu Ala

130	135	140
Gly Arg Glu Gln Tyr	Gly Arg Ala Gly Phe Ala	Gly Ser Tyr Ser Ser
145	150	155
Pro Tyr Pro Ala Tyr	Met Ala Asp Val Gly Ala	Ser Trp Ala Ala Ala
165	170	175
Ala Ala Ala Ser Ala	Gly Pro Phe Asp Ser Pro	Val Leu His Ser Leu
180	185	190
Pro Gly Arg Ala Asn	Pro Ala Ala Arg His Pro	Asn Leu Asp Met Phe
195	200	205
Asp Asp Phe Ser Glu	Gly Arg Glu Cys Val Asn	Cys Gly Ala Met Ser
210	215	220
Thr Pro Leu Trp Arg	Arg Asp Gly Thr Gly His	Tyr Leu Cys Asn Ala
225	230	235
Cys Gly Leu Tyr His	Lys Met Asn Gly Ile Asn	Arg Pro Leu Ile Lys
245	250	255
Pro Gln Arg Arg Leu	Ser Ala Ser Arg Arg Val	Gly Leu Ser Cys Ala
260	265	270
Asn Cys Gln Thr Thr	Thr Thr Thr Leu Trp Arg	Arg Asn Ala Glu Gly
275	280	285
Glu Pro Val Cys Asn	Ala Cys Gly Leu Tyr Met	Lys Leu His Gly Val
290	295	300
Pro Arg Pro Leu Ala	Met Arg Lys Glu Gly Ile	Gln Thr Arg Lys Arg
305	310	315
Lys Pro Lys Asn Leu	Asn Lys Ser Lys Thr Pro	Ala Ala Pro Ser Gly
325	330	335
Ser Glu Ser Leu Pro	Pro Ala Ser Gly Ala Ser	Ser Ser Asn Ser Ser Asn
340	345	350
Ala Thr Thr Ser Ser	Ser Glu Glu Met Arg Pro	Ile Lys Thr Glu Pro
355	360	365
Gly Leu Ser Ser His	Tyr Gly His Ser Ser Ser	Val Ser Gln Thr Phe
370	375	380
Ser Val Ser Ala Met	Ser Gly His Gly Pro Ser	Ile His Pro Val Leu
385	390	395
Ser Ala Leu Lys Leu	Ser Pro Gln Gly Tyr Ala	Ser Pro Val Ser Gln
405	410	415
Ser Pro Gln Thr Ser	Ser Ser Lys Gln Asp Ser	Trp Asn Ser Leu Val Leu

420 425 430
 Ala Asp Ser His Gly Asp Ile Ile Thr Ala
 435 440
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 <211> 1326
 <212> DNA
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 <221> CDS
 <223> (1)..(1329)
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 Met Tyr Gln Ser Leu Ala Met Ala Ala Asn His Gly Pro Pro Pro Gly
 1 5 10 15
 gcc tac cag gcg ggc ggc ccc ggc ccc ttc atg cac ggc gcg ggc gcc 96
 Ala Tyr Gln Ala Gly Gly Pro Gly Pro Phe Met His Gly Ala Gly Ala
 20 25 30
 gcg tcc tcg cca gtc tac ctg ccc aca ccg cgg gtg ccc tcc tcc gtt 144
 Ala Ser Ser Pro Val Tyr Leu Pro Thr Pro Arg Val Pro Ser Ser Val
 35 40 45
 ctg ggc ctg tcc tac ctc cag ggc gga ggc gcg ggc tct gcg tcc gga 192
 Leu Gly Leu Ser Tyr Leu Gln Gly Gly Gly Ala Gly Ser Ala Ser Gly
 50 55 60
 ggc ccc tcg ggc ggc agc ccc ggt ggg gcc gcg tct ggt gcg ggg ccc 240
 Gly Pro Ser Gly Gly Ser Pro Gly Gly Ala Ala Ser Gly Ala Gly Pro
 65 70 75 80
 ggg acc cag cag ggc agc ccg gga tgg agc cag gcg gga gcg acc gga 288
 Gly Thr Gln Gln Gly Ser Pro Gly Trp Ser Gln Ala Gly Ala Thr Gly
 85 90 95
 gcc gct tac acc ccg ccg ccg gtg tcg ccg cgc ttc tcc ttc ccg ggg 336
 Ala Ala Tyr Thr Pro Pro Pro Val Ser Pro Arg Phe Ser Phe Pro Gly
 100 105 110
 acc acc ggg tcc ctg gcg gcg gcg gcg gct gcc gcc gcc ccg gaa 384
 Thr Thr Gly Ser Leu Ala Ala Ala Ala Ala Ala Ala Ala Arg Glu
 115 120 125
 gct gcg gcc tac agc agt ggc ggc gga gcg gcg ggt gcg ggc ctg gcg 432

Ala Ala Ala Tyr Ser Ser Gly Gly Gly Ala Ala Gly Ala Gly Leu Ala
 130 135 140
 ggc cgc gag cag tac ggg cgc gcc ggc ttc gcg ggc tcc tac tcc agc 480
 Gly Arg Glu Gln Tyr Gly Arg Ala Gly Phe Ala Gly Ser Tyr Ser Ser
 145 150 155 160
 ccc tac cgc gct tac atg gcc gac gtg ggc gcg tcc tgg gcc gca gcc 528
 Pro Tyr Pro Ala Tyr Met Ala Asp Val Gly Ala Ser Trp Ala Ala Ala
 165 170 175
 gcc gcc gcc tcc gcc ggc ccc ttc gac agc ccg gtc ctg cac agc ctg 576
 Ala Ala Ala Ser Ala Gly Pro Phe Asp Ser Pro Val Leu His Ser Leu
 180 185 190
 ccc ggc cgg gcc aac ccg gcc gcc cga cac ccc aat ctc gat atg ttt 624
 Pro Gly Arg Ala Asn Pro Ala Ala Arg His Pro Asn Leu Asp Met Phe
 195 200 205
 gac gac ttc tca gaa ggc aga gag tgt gtc aac tgt ggg gct atg tcc 672
 Asp Asp Phe Ser Glu Gly Arg Glu Cys Val Asn Cys Gly Ala Met Ser
 210 215 220
 acc ccg ctc tgg agg cga gat ggg acg ggt cac tat ctg tgc aac gcc 720
 Thr Pro Leu Trp Arg Arg Asp Gly Thr Gly His Tyr Leu Cys Asn Ala
 225 230 235 240
 tgt ggc ctc tac cac aag atg aac ggc atc aac cgg ccg ctc atc aag 768
 Cys Gly Leu Tyr His Lys Met Asn Gly Ile Asn Arg Pro Leu Ile Lys
 245 250 255
 cct cag cgc cgg ctg tcc gcc tcc cgc cga gtg ggc ctc tcc tgt gcc 816
 Pro Gln Arg Arg Leu Ser Ala Ser Arg Arg Val Gly Leu Ser Cys Ala
 260 265 270
 aac tgc cag acc acc acc acc acc acg ctg tgg cgc cgc aat gcg gag ggc 864
 Asn Cys Gln Thr Thr Thr Thr Thr Leu Trp Arg Arg Asn Ala Glu Gly
 275 280 285
 gag cct gtg tgc aat gcc tgc ggc ctc tac atg aag ctc cac ggg gtg 912
 Glu Pro Val Cys Asn Ala Cys Gly Leu Tyr Met Lys Leu His Gly Val
 290 295 300
 ccc agg cct ctt gca atg cgg aaa gag ggg atc caa acc aga aaa cgg 960
 Pro Arg Pro Leu Ala Met Arg Lys Glu Gly Ile Gln Thr Arg Lys Arg
 305 310 315 320
 aag ccc aag aac ctg aat aaa tct aag aca cca gca gct cct tca ggc 1008

Lys Pro Lys Asn Leu Asn Lys Ser Lys Thr Pro Ala Ala Pro Ser Gly
 325 330 335
 agt gag agc ctt cct ccc gcc agc ggt gct tcc agc aac tcc agc aac 1056
 Ser Glu Ser Leu Pro Pro Ala Ser Gly Ala Ser Ser Asn Ser Ser Asn
 340 345 350
 gcc acc acc agc agc agc gag gag atg cgt ccc atc aag acg gag cct 1104
 Ala Thr Thr Ser Ser Ser Glu Glu Met Arg Pro Ile Lys Thr Glu Pro
 355 360 365
 ggc ctg tca tct cac tac ggg cac agc agc tcc gtg tcc cag acg ttc 1152
 Gly Leu Ser Ser His Tyr Gly His Ser Ser Ser Val Ser Gln Thr Phe
 370 375 380
 tca gtc agt gcg atg tct ggc cat ggg ccc tcc atc cac cct gtc ctc 1200
 Ser Val Ser Ala Met Ser Gly His Gly Pro Ser Ile His Pro Val Leu
 385 390 395 400
 tcg gcc ctg aag ctc tcc cca caa ggc tat gcg tct ccc gtc agc cag 1248
 Ser Ala Leu Lys Leu Ser Pro Gln Gly Tyr Ala Ser Pro Val Ser Gln
 405 410 415
 tct cca cag acc agc tcc aag cag gac tct tgg aac agt ctg gtc ttg 1296
 Ser Pro Gln Thr Ser Ser Lys Gln Asp Ser Trp Asn Ser Leu Val Leu
 420 425 430
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 Ala Asp Ser His Gly Asp Ile Ile Thr Ala
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 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60

Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys
 85 90 95
 Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu
 100 105 110
 Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn
 115 120 125
 His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val
 130 135 140
 Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly
 145 150 155 160
 Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp
 165 170 175
 Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser
 180 185 190
 Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met
 195 200 205
 Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro
 210 215 220
 Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly
 225 230 235 240
 Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro
 245 250 255
 Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp
 260 265 270
 Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu
 275 280 285
 Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser
 290 295 300
 Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro
 305 310 315 320
 Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr
 325 330 335
 Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly
 340 345 350

Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln
 355 360 365
 Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly
 370 375 380
 Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile
 385 390 395 400
 Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro
 405 410 415
 Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro
 420 425 430
 Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln
 435 440 445
 Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser
 450 455 460
 Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro
 465 470 475 480
 Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser
 485 490 495
 Val Lys Arg Met Arg Met Asp Ala Trp Val Thr
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<210> 14

<211> 1521

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1524)

<400> 14

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Met	Gly	Arg	Lys	Lys	Ile	Gln	Ile	Thr	Arg	Ile	Met	Asp	Glu	Arg	Asn	
1				5					10					15		
cga	cag	gtc	act	ttt	aca	aag	aga	aag	ttt	gga	tta	atg	aag	aaa	gcc	96
Arg	Gln	Val	Thr	Phe	Thr	Lys	Arg	Lys	Phe	Gly	Leu	Met	Lys	Lys	Ala	
			20						25					30		
tat	gaa	ctt	agt	gtg	ctc	tgt	gac	tgt	gaa	ata	gca	ctc	atc	att	ttc	144
Tyr	Glu	Leu	Ser	Val	Leu	Cys	Asp	Cys	Glu	Ile	Ala	Leu	Ile	Ile	Phe	

35	40	45	
aac agc tct aac aaa ctg ttt caa tat gct agc act gat atg gac aaa			192
Asn Ser Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys			
50	55	60	
gtt ctt ctc aag tat aca gaa tat aat gaa cct cat gaa agc aga acc			240
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr			
65	70	75	80
aac tcg gat att gtt gag gct ctg aac aag aag gaa cac aga ggg tgc			288
Asn Ser Asp Ile Val Glu Ala Leu Asn Lys Lys Glu His Arg Gly Cys			
85	90	95	
gac agc cca gac cct gat act tca tat gtg cta act cca cat aca gaa			336
Asp Ser Pro Asp Pro Asp Thr Ser Tyr Val Leu Thr Pro His Thr Glu			
100	105	110	
gaa aaa tat aaa aaa att aat gag gaa ttt gat aat atg atg egg aat			384
Glu Lys Tyr Lys Lys Ile Asn Glu Glu Phe Asp Asn Met Met Arg Asn			
115	120	125	
cat aaa atc gca cct ggt ctg cca cct cag aac ttt tca atg tct gtc			432
His Lys Ile Ala Pro Gly Leu Pro Pro Gln Asn Phe Ser Met Ser Val			
130	135	140	
aca gtt cca gtg acc agc ccc aat gct ttg tcc tac act aac cca ggg			480
Thr Val Pro Val Thr Ser Pro Asn Ala Leu Ser Tyr Thr Asn Pro Gly			
145	150	155	160
agt tca ctg gtg tcc cca tct ttg gca gcc agc tca acg tta aca gat			528
Ser Ser Leu Val Ser Pro Ser Leu Ala Ala Ser Ser Thr Leu Thr Asp			
165	170	175	
tca agc atg ctc tct cca cct caa acc aca tta cat aga aat gtg tct			576
Ser Ser Met Leu Ser Pro Pro Gln Thr Thr Leu His Arg Asn Val Ser			
180	185	190	
cct gga gct cct cag aga cca cca agt act ggc aat gca ggt ggg atg			624
Pro Gly Ala Pro Gln Arg Pro Pro Ser Thr Gly Asn Ala Gly Gly Met			
195	200	205	
ttg agc act aca gac ctc aca gtg cca aat gga gct gga agc agt cca			672
Leu Ser Thr Thr Asp Leu Thr Val Pro Asn Gly Ala Gly Ser Ser Pro			
210	215	220	
gtg ggg aat gga ttt gta aac tca aga gct tct cca aat ttg att gga			720
Val Gly Asn Gly Phe Val Asn Ser Arg Ala Ser Pro Asn Leu Ile Gly			

225	230	235	240	
gct act ggt gca aat agc tta ggc aaa gtc atg cct aca aag tct ccc				768
Ala Thr Gly Ala Asn Ser Leu Gly Lys Val Met Pro Thr Lys Ser Pro				
	245	250	255	
cct cca cca ggt ggt ggt aat ctt gga atg aac agt agg aaa cca gat				816
Pro Pro Pro Gly Gly Gly Asn Leu Gly Met Asn Ser Arg Lys Pro Asp				
	260	265	270	
ctt cga gtt gtc atc ccc cct tca agc aag ggc atg atg cct cca cta				864
Leu Arg Val Val Ile Pro Pro Ser Ser Lys Gly Met Met Pro Pro Leu				
	275	280	285	
tcg gag gaa gag gaa ttg gag ttg aac acc caa agg atc agt agt tct				912
Ser Glu Glu Glu Glu Leu Glu Leu Asn Thr Gln Arg Ile Ser Ser Ser				
	290	295	300	
caa gcc act caa cct ctt get acc cca gtc gtg tct gtg aca acc cca				960
Gln Ala Thr Gln Pro Leu Ala Thr Pro Val Val Ser Val Thr Thr Pro				
305	310	315	320	
agc ttg cct ccg caa gga ctt gtg tac tca gca atg ccg act gcc tac				1008
Ser Leu Pro Pro Gln Gly Leu Val Tyr Ser Ala Met Pro Thr Ala Tyr				
	325	330	335	
aac act gat tat tca ctg acc agc gct gac ctg tca gcc ctt caa ggc				1056
Asn Thr Asp Tyr Ser Leu Thr Ser Ala Asp Leu Ser Ala Leu Gln Gly				
	340	345	350	
ttc aac tcg cca gga atg ctg tcg ctg gga cag gtg tcg gcc tgg cag				1104
Phe Asn Ser Pro Gly Met Leu Ser Leu Gly Gln Val Ser Ala Trp Gln				
	355	360	365	
cag cac cac cta gga caa gca gcc ctc agc tct ctt gtt gct gga ggg				1152
Gln His His Leu Gly Gln Ala Ala Leu Ser Ser Leu Val Ala Gly Gly				
	370	375	380	
cag tta tct cag ggt tcc aat tta tcc att aat acc aac caa aac atc				1200
Gln Leu Ser Gln Gly Ser Asn Leu Ser Ile Asn Thr Asn Gln Asn Ile				
385	390	395	400	
agc atc aag tcc gaa ccg att tca cct cct cgg gat cgt atg acc cca				1248
Ser Ile Lys Ser Glu Pro Ile Ser Pro Pro Arg Asp Arg Met Thr Pro				
	405	410	415	
tcg ggc ttc cag cag cag cag cag cag cag cag cag cag cag cag cag				1296
Ser Gly Phe Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Pro Pro				

420	425	430	
cca cca ccg cag ccc cag cca caa ccc ccg cag ccc cag ccc cga cag			1344
Pro Pro Pro Gln Pro Gln Pro Gln Pro Pro Gln Pro Gln Pro Arg Gln			
435	440	445	
gaa atg ggg cgc tcc cct gtg gac agt ctg agc agc tct agt agc tcc			1392
Glu Met Gly Arg Ser Pro Val Asp Ser Leu Ser Ser Ser Ser Ser Ser			
450	455	460	
tat gat ggc agt gat cgg gag gat cca cgg ggc gac ttc cat tct cca			1440
Tyr Asp Gly Ser Asp Arg Glu Asp Pro Arg Gly Asp Phe His Ser Pro			
465	470	475	480
att gtg ctt ggc cga ccc cca aac act gag gac aga gaa agc cct tct			1488
Ile Val Leu Gly Arg Pro Pro Asn Thr Glu Asp Arg Glu Ser Pro Ser			
485	490	495	
gta aag cga atg agg atg gac gcg tgg gtg acc			1521
Val Lys Arg Met Arg Met Asp Ala Trp Val Thr			
500	505		

<210> 15

<211> 365

<212> PRT

<213> Homo sapiens

<400> 15

Met Gly Arg Lys Lys Ile Gln Ile Ser Arg Ile Leu Asp Gln Arg Asn

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10

15

Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala

20

25

30

Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe

35

40

45

Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg

50

55

60

Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr

65

70

75

80

Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp

85

90

95

Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys

100

105

110

Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp Pro Ala Leu Pro Arg Pro

115 120 125
 Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr
 130 135 140
 Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala
 145 150 155 160
 Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys
 165 170 175
 Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu
 180 185 190
 Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg
 195 200 205
 Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr
 210 215 220
 Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr
 225 230 235 240
 Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro
 245 250 255
 Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro
 260 265 270
 Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg
 275 280 285
 Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys
 290 295 300
 Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys
 305 310 315 320
 Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly
 325 330 335
 Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr Ala Arg Ala Arg Gly Asp
 340 345 350
 Pro Thr Ser Leu Gln Ala Ser Ser Glu Lys Thr Gln Gln
 355 360

<210> 16

<211> 1095

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1098)

<400> 16

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cgg cag gtg acg ttc acc aag cgg aag ttc ggg ctg atg aag aag gcc	96
Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala	
20 25 30	
tat gag ctg agc gtg ctc tgt gac tgt gag ata gcc ctc atc atc ttc	144
Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe	
35 40 45	
aac agc gcc aac cgc ctc ttc cag tat gcc agc acg gac atg gac cgt	192
Asn Ser Ala Asn Arg Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Arg	
50 55 60	
gtg ctg ctg aag tac aca gag tac agc gag ccc cac gag agc cgc acc	240
Val Leu Leu Lys Tyr Thr Glu Tyr Ser Glu Pro His Glu Ser Arg Thr	
65 70 75 80	
aac act gac atc ctc gag acg ctg aag cgg agg ggc att ggc ctc gat	288
Asn Thr Asp Ile Leu Glu Thr Leu Lys Arg Arg Gly Ile Gly Leu Asp	
85 90 95	
ggg cca gag ctg gag cgg gat gaa ggg cct gag gag cca gga gag aag	336
Gly Pro Glu Leu Glu Pro Asp Glu Gly Pro Glu Glu Pro Gly Glu Lys	
100 105 110	
ttt cgg agg ctg gca ggc gaa ggg ggt gat ccg gcc ttg ccc cga ccc	384
Phe Arg Arg Leu Ala Gly Glu Gly Gly Asp Pro Ala Leu Pro Arg Pro	
115 120 125	
cgg ctg tat cct gca gct cct gct atg ccc agc cca gat gtg gta tac	432
Arg Leu Tyr Pro Ala Ala Pro Ala Met Pro Ser Pro Asp Val Val Tyr	
130 135 140	
ggg gcc tta ccg cca cca ggc tgt gac ccc agt ggg ctt ggg gaa gca	480
Gly Ala Leu Pro Pro Pro Gly Cys Asp Pro Ser Gly Leu Gly Glu Ala	
145 150 155 160	
ctg ccc gcc cag agc cgc cca tct ccc ttc cga cca gca gcc ccc aaa	528
Leu Pro Ala Gln Ser Arg Pro Ser Pro Phe Arg Pro Ala Ala Pro Lys	
165 170 175	

gcc ggg ccc cca ggc ctg gtg cac cct ctc ttc tca cca agc cac ctc 576
 Ala Gly Pro Pro Gly Leu Val His Pro Leu Phe Ser Pro Ser His Leu
 180 185 190
 acc agc aag aca cca ccc cca ctg tac ctg ccg acg gaa ggg cgg agg 624
 Thr Ser Lys Thr Pro Pro Pro Leu Tyr Leu Pro Thr Glu Gly Arg Arg
 195 200 205
 tca gac ctg cct ggt ggc ctg gct ggg ccc cga ggg gga cta aac acc 672
 Ser Asp Leu Pro Gly Gly Leu Ala Gly Pro Arg Gly Gly Leu Asn Thr
 210 215 220
 tcc aga agc ctc tac agt ggc ctg cag aac ccc tgc tcc act gca act 720
 Ser Arg Ser Leu Tyr Ser Gly Leu Gln Asn Pro Cys Ser Thr Ala Thr
 225 230 235 240
 ccc gga ccc cca ctg ggg agc ttc ccc ttc ctc ccc gga ggc ccc cca 768
 Pro Gly Pro Pro Leu Gly Ser Phe Pro Phe Leu Pro Gly Gly Pro Pro
 245 250 255
 gtg ggg gcc gaa gcc tgg gcg agg agg gtc ccc caa ccc gcg gcg cct 816
 Val Gly Ala Glu Ala Trp Ala Arg Arg Val Pro Gln Pro Ala Ala Pro
 260 265 270
 ccc cgc cga ccc ccc cag tca gca tca agt ctg agc gcc tct ctc cgg 864
 Pro Arg Arg Pro Pro Gln Ser Ala Ser Ser Leu Ser Ala Ser Leu Arg
 275 280 285
 ccc ccg ggg gcc ccg gcg act ttc cta aga cct tcc cct atc cct tgc 912
 Pro Pro Gly Ala Pro Ala Thr Phe Leu Arg Pro Ser Pro Ile Pro Cys
 290 295 300
 tcc tcg ccc ggt ccc tgg cag agc ctc tgc ggc ctg ggc ccg ccc tgc 960
 Ser Ser Pro Gly Pro Trp Gln Ser Leu Cys Gly Leu Gly Pro Pro Cys
 305 310 315 320
 gcc ggc tgc cct tgg ccg acg gct ggc ccc ggt agg aga tca ccc ggt 1008
 Ala Gly Cys Pro Trp Pro Thr Ala Gly Pro Gly Arg Arg Ser Pro Gly
 325 330 335
 ggc acc agc cca gag cgc tcg cca ggt acg gcg agg gca cgt ggg gac 1056
 Gly Thr Ser Pro Glu Arg Ser Pro Gly Thr Ala Arg Ala Arg Gly Asp
 340 345 350
 ccc acc tcc ctc cag gcc tct tca gag aag acc caa cag 1095
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 355 360 365

<210> 17

<211> 465

<212> PRT

<213> Homo sapiens

<400> 17

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 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 Asn Ser Asp Ile Val Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys
 85 90 95
 Asp Ser Pro Asp Pro Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu
 100 105 110
 Ser Glu Asp Lys Tyr Arg Lys Ile Asn Glu Asp Ile Asp Leu Met Ile
 115 120 125
 Ser Arg Gln Arg Leu Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro
 130 135 140
 Val Ser Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro
 145 150 155 160
 Val Ser Ser Leu Gly Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser
 165 170 175
 Leu Gln Arg Asn Ser Met Ser Pro Gly Val Thr His Arg Pro Pro Ser
 180 185 190
 Ala Gly Asn Thr Gly Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala
 195 200 205
 Gly Thr Ser Ala Gly Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly
 210 215 220
 Leu Leu Val Ser Pro Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser
 225 230 235 240
 Pro Pro Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg

245 250 255
 Val Leu Ile Pro Pro Gly Ser Lys Asn Thr Met Pro Ser Val Asn Gln
 260 265 270
 Arg Ile Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr Pro Val Val
 275 280 285
 Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly Gly Tyr Pro
 290 295 300
 Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu Ser Ser Ala
 305 310 315 320
 Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala Leu His Leu
 325 330 335
 Gly Ser Val Thr Gly Trp Gln Gln Gln His Leu His Asn Met Pro Pro
 340 345 350
 Ser Ala Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His Leu Ser Gln
 355 360 365
 Ser Ser Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn Ile Lys Ser
 370 375 380
 Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro Ser Arg Tyr
 385 390 395 400
 Pro Gln His Thr Arg His Glu Ala Gly Arg Ser Pro Val Asp Ser Leu
 405 410 415
 Ser Ser Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu Asp His Arg
 420 425 430
 Asn Glu Phe His Ser Pro Ile Gly Leu Thr Arg Pro Ser Pro Asp Glu
 435 440 445
 Arg Glu Ser Pro Ser Val Lys Arg Met Arg Leu Ser Glu Gly Trp Ala
 450 455 460

Thr

<210> 18

<211> 1395

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1398)

<400> 18

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 Met Gly Arg Lys Lys Ile Gln Ile Thr Arg Ile Met Asp Glu Arg Asn
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 aga cag gtg aca ttt aca aag agg aaa ttt ggg ttg atg aag aag gct 96
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 tat gag ctg agc gtg ctg tgt gac tgt gag att gcg ctg atc atc ttc 144
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 aac agc acc aac aag ctg ttc cag tat gcc agc acc gac atg gac aaa 192
 Asn Ser Thr Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 gtg ctt ctc aag tac acg gag tac aac gag ccg cat gag agc cgg aca 240
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 aac tca gac atc gtg gag acg ttg aga aag aag ggc ctt aat ggc tgt 288
 Asn Ser Asp Ile Val Glu Thr Leu Arg Lys Lys Gly Leu Asn Gly Cys
 85 90 95
 gac agc cca gac ccc gat gcg gac gat tcc gta ggt cac agc cct gag 336
 Asp Ser Pro Asp Pro Asp Ala Asp Asp Ser Val Gly His Ser Pro Glu
 100 105 110
 tct gag gac aag tac agg aaa att aac gaa gat att gat cta atg atc 384
 Ser Glu Asp Lys Tyr Arg Lys Ile Asn Glu Asp Ile Asp Leu Met Ile
 115 120 125
 agc agg caa aga ttg tgt gct gtt cca cct ccc aac ttc gag atg cca 432
 Ser Arg Gln Arg Leu Cys Ala Val Pro Pro Pro Asn Phe Glu Met Pro
 130 135 140
 gtc tcc atc cca gtg tcc agc cac aac agt ttg gtg tac agc aac cct 480
 Val Ser Ile Pro Val Ser Ser His Asn Ser Leu Val Tyr Ser Asn Pro
 145 150 155 160
 gtc agc tca ctg gga aac ccc aac cta ttg cca ctg gct cac cct tct 528
 Val Ser Ser Leu Gly Asn Pro Asn Leu Leu Pro Leu Ala His Pro Ser
 165 170 175
 ctg cag agg aat agt atg tct cct ggt gta aca cat cga cct cca agt 576
 Leu Gln Arg Asn Ser Met Ser Pro Gly Val Thr His Arg Pro Pro Ser
 180 185 190

gca ggt aac aca ggt ggt ctg atg ggt gga gac etc acg tct ggt gca 624
 Ala Gly Asn Thr Gly Gly Leu Met Gly Gly Asp Leu Thr Ser Gly Ala
 195 200 205
 ggc acc agt gca ggg aac ggg tat ggc aat ccc cga aac tca cca ggt 672
 Gly Thr Ser Ala Gly Asn Gly Tyr Gly Asn Pro Arg Asn Ser Pro Gly
 210 215 220
 ctg ctg gtc tca cct ggt aac ttg aac aag aat atg caa gca aaa tct 720
 Leu Leu Val Ser Pro Gly Asn Leu Asn Lys Asn Met Gln Ala Lys Ser
 225 230 235 240
 cct ccc cca atg aat tta gga atg aat aac cgt aaa cca gat etc cga 768
 Pro Pro Pro Met Asn Leu Gly Met Asn Asn Arg Lys Pro Asp Leu Arg
 245 250 255
 gtt ctt att cca cca ggc agc aag aat acg atg cca tca gtg aat caa 816
 Val Leu Ile Pro Pro Gly Ser Lys Asn Thr Met Pro Ser Val Asn Gln
 260 265 270
 agg ata aat aac tcc cag tgc gct cag tca ttg gct acc cca gtg gtt 864
 Arg Ile Asn Asn Ser Gln Ser Ala Gln Ser Leu Ala Thr Pro Val Val
 275 280 285
 tcc gta gca act cct act tta cca gga caa gga atg gga gga tat cca 912
 Ser Val Ala Thr Pro Thr Leu Pro Gly Gln Gly Met Gly Gly Tyr Pro
 290 295 300
 tca gcc att tca aca aca tat ggt acc gag tac tct ctg agt agt gca 960
 Ser Ala Ile Ser Thr Thr Tyr Gly Thr Glu Tyr Ser Leu Ser Ser Ala
 305 310 315 320
 gac ctg tca tct ctg tct ggg ttt aac acc gcc agc gct ctt cac ctt 1008
 Asp Leu Ser Ser Leu Ser Gly Phe Asn Thr Ala Ser Ala Leu His Leu
 325 330 335
 ggt tca gta act ggc tgg caa cag caa cac cta cat aac atg cca cca 1056
 Gly Ser Val Thr Gly Trp Gln Gln Gln His Leu His Asn Met Pro Pro
 340 345 350
 tct gcc etc agt cag ttg gga gct tgc act agc act cat tta tct cag 1104
 Ser Ala Leu Ser Gln Leu Gly Ala Cys Thr Ser Thr His Leu Ser Gln
 355 360 365
 agt tca aat etc tcc ctg cct tct act caa agc etc aac atc aag tca 1152
 Ser Ser Asn Leu Ser Leu Pro Ser Thr Gln Ser Leu Asn Ile Lys Ser
 370 375 380

gaa cct gtt tct cct cct aga gac cgt acc acc acc cct tcg aga tac 1200
 Glu Pro Val Ser Pro Pro Arg Asp Arg Thr Thr Thr Pro Ser Arg Tyr
 385 390 395 400
 cca caa cac acg cgc cac gag gcg ggg aga tct cct gtt gac agc ttg 1248
 Pro Gln His Thr Arg His Glu Ala Gly Arg Ser Pro Val Asp Ser Leu
 405 410 415
 agc agc tgt agc agt tcg tac gac ggg agc gac cga gag gat cac cgg 1296
 Ser Ser Cys Ser Ser Ser Tyr Asp Gly Ser Asp Arg Glu Asp His Arg
 420 425 430
 aac gaa ttc cac tcc ccc att gga ctc acc aga cct tcg ccg gac gaa 1344
 Asn Glu Phe His Ser Pro Ile Gly Leu Thr Arg Pro Ser Pro Asp Glu
 435 440 445
 agg gaa agt ccc tca gtc aag cgc atg cga ctt tct gaa gga tgg gca 1392
 Arg Glu Ser Pro Ser Val Lys Arg Met Arg Leu Ser Glu Gly Trp Ala
 450 455 460
 aca 1395
 Thr
 465
 <210> 19
 <211> 521
 <212> PRT
 <213> Homo sapiens
 <400> 19
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 1 5 10 15
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys
 50 55 60
 Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr
 65 70 75 80
 Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly Phe Asn Gly Cys
 85 90 95
 Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu Gln Ser Pro Leu

100 105 110
 Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe
 115 120 125
 Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe Ala Met Pro Val
 130 135 140
 Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe Ser Asn Pro Ser
 145 150 155 160
 Gly Ser Leu Val Thr Pro Ser Leu Val Thr Ser Ser Leu Thr Asp Pro
 165 170 175
 Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg Asn Ser Val Ser
 180 185 190
 Pro Gly Leu Pro Gln Arg Pro Ala Ser Ala Gly Ala Met Leu Gly Gly
 195 200 205
 Asp Leu Asn Ser Ala Asn Gly Ala Cys Pro Ser Pro Val Gly Asn Gly
 210 215 220
 Tyr Val Ser Ala Arg Ala Ser Pro Gly Leu Leu Pro Val Ala Asn Gly
 225 230 235 240
 Asn Ser Leu Asn Lys Val Ile Pro Ala Lys Ser Pro Pro Pro Pro Thr
 245 250 255
 His Ser Thr Gln Leu Gly Ala Pro Ser Arg Lys Pro Asp Leu Arg Val
 260 265 270
 Ile Thr Ser Gln Ala Gly Lys Gly Leu Met His His Leu Thr Glu Asp
 275 280 285
 His Leu Asp Leu Asn Asn Ala Gln Arg Leu Gly Val Ser Gln Ser Thr
 290 295 300
 His Ser Leu Thr Thr Pro Val Val Ser Val Ala Thr Pro Ser Leu Leu
 305 310 315 320
 Ser Gln Gly Leu Pro Phe Ser Ser Met Pro Thr Ala Tyr Asn Thr Asp
 325 330 335
 Tyr Gln Leu Thr Ser Ala Glu Leu Ser Ser Leu Pro Ala Phe Ser Ser
 340 345 350
 Pro Gly Gly Leu Ser Leu Gly Asn Val Thr Ala Trp Gln Gln Pro Gln
 355 360 365
 Gln Pro Gln Gln Pro Gln Gln Pro Gln Pro Pro Gln Gln Gln Pro Pro
 370 375 380
 Gln Pro Gln Gln Pro Gln Pro Gln Gln Pro Gln Gln Pro Gln Gln Pro

385 390 395 400
 Pro Gln Gln Gln Ser His Leu Val Pro Val Ser Leu Ser Asn Leu Ile
 405 410 415
 Pro Gly Ser Pro Leu Pro His Val Gly Ala Ala Leu Thr Val Thr Thr
 420 425 430
 His Pro His Ile Ser Ile Lys Ser Glu Pro Val Ser Pro Ser Arg Glu
 435 440 445
 Arg Ser Pro Ala Pro Pro Pro Pro Ala Val Phe Pro Ala Ala Arg Pro
 450 455 460
 Glu Pro Gly Asp Gly Leu Ser Ser Pro Ala Gly Gly Ser Tyr Glu Thr
 465 470 475 480
 Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro Thr Leu Gly Leu
 485 490 495
 Leu Arg Pro Ala Pro Glu Pro Glu Ala Glu Gly Ser Ala Val Lys Arg
 500 505 510
 Met Arg Leu Asp Thr Trp Thr Leu Lys
 515 520

<210> 20

<211> 1563

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1566)

<400> 20

atg ggg agg aaa aag att cag atc cag cga atc acc gac gag cgg aac 48
 Met Gly Arg Lys Lys Ile Gln Ile Gln Arg Ile Thr Asp Glu Arg Asn
 1 5 10 15
 cga cag gtg act ttc acc aag cgg aag ttt ggc ctg atg aag aag gcg 96
 Arg Gln Val Thr Phe Thr Lys Arg Lys Phe Gly Leu Met Lys Lys Ala
 20 25 30
 tat gag ctg agc gtg cta tgt gac tgc gag atc gca ctc atc atc ttc 144
 Tyr Glu Leu Ser Val Leu Cys Asp Cys Glu Ile Ala Leu Ile Ile Phe
 35 40 45
 aac cac tcc aac aag ctg ttc cag tac gcc agc acc gac atg gac aag 192
 Asn His Ser Asn Lys Leu Phe Gln Tyr Ala Ser Thr Asp Met Asp Lys

50	55	60	
gtg ctg ctc aag tac acg gag tac aat gag cca cac gag agc cgc acc			240
Val Leu Leu Lys Tyr Thr Glu Tyr Asn Glu Pro His Glu Ser Arg Thr			
65	70	75	80
aac gcc gac atc atc gag acc ctg agg aag aag ggc ttc aat ggc tgc			288
Asn Ala Asp Ile Ile Glu Thr Leu Arg Lys Lys Gly Phe Asn Gly Cys			
85	90	95	
gac agc ccc gag ccc gac ggg gag gac tgc ctg gaa cag agc ccc ctg			336
Asp Ser Pro Glu Pro Asp Gly Glu Asp Ser Leu Glu Gln Ser Pro Leu			
100	105	110	
ctg gag gac aag tac cga cgc gcc agc gag gag ctc gac ggg ctc ttc			384
Leu Glu Asp Lys Tyr Arg Arg Ala Ser Glu Glu Leu Asp Gly Leu Phe			
115	120	125	
cgg cgc tat ggg tca act gtc ccg gcc ccc aac ttt gcc atg cct gtc			432
Arg Arg Tyr Gly Ser Thr Val Pro Ala Pro Asn Phe Ala Met Pro Val			
130	135	140	
acg gtg ccc gtg tcc aat cag agc tca ctg cag ttc agc aat ccc agc			480
Thr Val Pro Val Ser Asn Gln Ser Ser Leu Gln Phe Ser Asn Pro Ser			
145	150	155	160
ggc tcc ctg gtc acc cct tcc ctg gtg aca tca tcc ctc acg gac ccg			528
Gly Ser Leu Val Thr Pro Ser Leu Val Thr Ser Ser Leu Thr Asp Pro			
165	170	175	
cgg ctc ctg tcc ccc cag cag cca gca cta cag agg aac agt gtg tct			576
Arg Leu Leu Ser Pro Gln Gln Pro Ala Leu Gln Arg Asn Ser Val Ser			
180	185	190	
cct ggc ctg ccc cag cgg cca gct agt gcg ggg gcc atg ctg ggg ggt			624
Pro Gly Leu Pro Gln Arg Pro Ala Ser Ala Gly Ala Met Leu Gly Gly			
195	200	205	
gac ctg aac agt gct aac gga gcc tgc ccc agc cct gtt ggg aat gcc			672
Asp Leu Asn Ser Ala Asn Gly Ala Cys Pro Ser Pro Val Gly Asn Gly			
210	215	220	
tac gtc agt gct cgg gct tcc cct ggc ctc ctc cct gtg gcc aat gcc			720
Tyr Val Ser Ala Arg Ala Ser Pro Gly Leu Leu Pro Val Ala Asn Gly			
225	230	235	240
aac agc cta aac aag gtc atc cct gcc aag tct ccg ccc cca cct acc			768
Asn Ser Leu Asn Lys Val Ile Pro Ala Lys Ser Pro Pro Pro Thr			

	245	250	255	
cac agc acc cag ctt gga gcc ccc agc cgc aag ccc gac ctg cga gtc				816
His Ser Thr Gln Leu Gly Ala Pro Ser Arg Lys Pro Asp Leu Arg Val				
	260	265	270	
atc act tcc cag gca gga aag ggg tta atg cat cac ttg act gag gac				864
Ile Thr Ser Gln Ala Gly Lys Gly Leu Met His His Leu Thr Glu Asp				
	275	280	285	
cat tta gat ctg aac aat gcc cag cgc ctt ggg gtc tcc cag tct act				912
His Leu Asp Leu Asn Asn Ala Gln Arg Leu Gly Val Ser Gln Ser Thr				
	290	295	300	
cat tcg ctc acc acc cca gtg gtt tct gtg gca acg ccg agt tta ctc				960
His Ser Leu Thr Thr Pro Val Val Ser Val Ala Thr Pro Ser Leu Leu				
	305	310	315	320
agc cag ggc ctc ccc ttc tct tcc atg ccc act gcc tac aac aca gat				1008
Ser Gln Gly Leu Pro Phe Ser Ser Met Pro Thr Ala Tyr Asn Thr Asp				
	325	330	335	
tac cag ttg acc agt gca gag ctc tcc tcc tta cca gcc ttt agt tca				1056
Tyr Gln Leu Thr Ser Ala Glu Leu Ser Ser Leu Pro Ala Phe Ser Ser				
	340	345	350	
cct ggg ggg ctg tcg cta ggc aat gtc act gcc tgg caa cag cca cag				1104
Pro Gly Gly Leu Ser Leu Gly Asn Val Thr Ala Trp Gln Gln Pro Gln				
	355	360	365	
cag ccc cag cag ccg cag cag cca cag cct cca cag cag cag cca ccg				1152
Gln Pro Gln Gln Pro Gln Gln Pro Gln Pro Pro Gln Gln Gln Pro Pro				
	370	375	380	
cag cca cag cag cca cag cca cag cag cct cag cag ccg caa cag cca				1200
Gln Pro Gln Gln Pro Gln Pro Gln Gln Pro Gln Gln Pro Gln Gln Pro				
	385	390	395	400
cct cag caa cag tcc cac ctg gtc cct gta tct ctc agc aac ctc atc				1248
Pro Gln Gln Gln Ser His Leu Val Pro Val Ser Leu Ser Asn Leu Ile				
	405	410	415	
ccg ggc agc ccc ctg ccc cac gtg ggt gct gcc ctc aca gtc acc acc				1296
Pro Gly Ser Pro Leu Pro His Val Gly Ala Ala Leu Thr Val Thr Thr				
	420	425	430	
cac ccc cac atc agc atc aag tca gaa ccg gtg tcc cca agc cgt gag				1344
His Pro His Ile Ser Ile Lys Ser Glu Pro Val Ser Pro Ser Arg Glu				

435 440 445
 cgc agc cct gcg cct ccc cct cca gct gtg ttc cca gct gcc cgc cct 1392
 Arg Ser Pro Ala Pro Pro Pro Pro Ala Val Phe Pro Ala Ala Arg Pro
 450 455 460
 gag cct ggc gat ggt ctc agc agc cca gcc ggg gga tcc tat gag acg 1440
 Glu Pro Gly Asp Gly Leu Ser Ser Pro Ala Gly Gly Ser Tyr Glu Thr
 465 470 475 480
 gga gac cgg gat gac gga cgg ggg gac ttc ggg ccc aca ctg ggc ctg 1488
 Gly Asp Arg Asp Asp Gly Arg Gly Asp Phe Gly Pro Thr Leu Gly Leu
 485 490 495
 ctg cgc cca gcc cca gag cct gag gct gag ggc tca gct gtg aag agg 1536
 Leu Arg Pro Ala Pro Glu Pro Glu Ala Glu Gly Ser Ala Val Lys Arg
 500 505 510
 atg egg ctt gat acc tgg aca tta aag 1563
 Met Arg Leu Asp Thr Trp Thr Leu Lys
 515 520
 <210> 21
 <211> 217
 <212> PRT
 <213> Rattus norvegicus
 <400> 21
 Met Ser Leu Val Gly Gly Phe Pro His His Pro Val Val His His Glu
 1 5 10 15
 Gly Tyr Pro Phe Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
 20 25 30
 Ser Arg Cys Ser His Glu Glu Asn Pro Tyr Phe His Gly Trp Leu Ile
 35 40 45
 Gly His Pro Glu Met Ser Pro Pro Asp Tyr Ser Met Ala Leu Ser Tyr
 50 55 60
 Ser Pro Glu Tyr Ala Ser Gly Ala Ala Gly Leu Asp His Ser His Tyr
 65 70 75 80
 Gly Gly Val Pro Pro Gly Ala Gly Pro Pro Gly Leu Gly Gly Pro Arg
 85 90 95
 Pro Val Lys Arg Arg Gly Thr Ala Asn Arg Lys Glu Arg Arg Arg Thr
 100 105 110
 Gln Ser Ile Asn Ser Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn

115 120 125
 Val Pro Ala Asp Thr Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala
 130 135 140
 Thr Ser Tyr Ile Ala Tyr Leu Met Asp Leu Leu Ala Lys Asp Asp Gln
 145 150 155 160
 Asn Gly Glu Ala Glu Ala Phe Lys Ala Glu Ile Lys Lys Thr Asp Val
 165 170 175
 Lys Glu Glu Lys Arg Lys Lys Glu Leu Asn Glu Ile Leu Lys Ser Thr
 180 185 190
 Val Ser Ser Asn Asp Lys Lys Thr Lys Gly Arg Thr Gly Trp Pro Gln
 195 200 205
 His Val Trp Ala Leu Glu Leu Lys Gln
 210 215

<210> 22

<211> 651

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<223> (1)..(654)

<400> 22

atg agt ctg gtg ggg ggc ttt ccc cac cac ccc gtg gtg cac cat gag 48
 Met Ser Leu Val Gly Gly Phe Pro His His Pro Val Val His His Glu
 1 5 10 15
 ggc tac ccg ttc gcc gca gcc gca gcc gcc gct gct gct gcc gcc gcc 96
 Gly Tyr Pro Phe Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala Ala
 20 25 30
 agc cgc tgc agt cac gag gag aac ccc tat ttc cac ggc tgg ctt att 144
 Ser Arg Cys Ser His Glu Glu Asn Pro Tyr Phe His Gly Trp Leu Ile
 35 40 45
 ggc cac ccg gag atg tcg ccc ccc gac tac agc atg gcc ctg tcc tac 192
 Gly His Pro Glu Met Ser Pro Pro Asp Tyr Ser Met Ala Leu Ser Tyr
 50 55 60
 agt ccc gag tac gcc agc ggt gcc gcg ggc ctg gac cac tcc cat tat 240
 Ser Pro Glu Tyr Ala Ser Gly Ala Ala Gly Leu Asp His Ser His Tyr
 65 70 75 80

ggg gga gtg ccg ccc ggt gcc ggg cct ccc ggc ctg ggg ggg ccg cgc 288
 Gly Gly Val Pro Pro Gly Ala Gly Pro Pro Gly Leu Gly Gly Pro Arg
 85 90 95
 ccg gtg aag cgt cgg ggc acc gcc aac cgc aag gag cgg cgc agg act 336
 Pro Val Lys Arg Arg Gly Thr Ala Asn Arg Lys Glu Arg Arg Arg Thr
 100 105 110
 cag agc atc aac agc gcc ttc gcc gag ctg cgc gag tgc atc ccc aac 384
 Gln Ser Ile Asn Ser Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn
 115 120 125
 gtg ccc gcc gac acc aaa ctc tcc aaa atc aag act ctg cgc ctg gcc 432
 Val Pro Ala Asp Thr Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala
 130 135 140
 acc agc tac atc gcc tac ctc atg gat ctg ctg gcc aag gac gac cag 480
 Thr Ser Tyr Ile Ala Tyr Leu Met Asp Leu Leu Ala Lys Asp Asp Gln
 145 150 155 160
 aac gga gag gcg gag gcc ttc aag gcg gag atc aag aag acc gac gtg 528
 Asn Gly Glu Ala Glu Ala Phe Lys Ala Glu Ile Lys Lys Thr Asp Val
 165 170 175
 aaa gag gag aag agg aag aaa gag ctg aat gaa atc ttg aaa agt aca 576
 Lys Glu Glu Lys Arg Lys Lys Glu Leu Asn Glu Ile Leu Lys Ser Thr
 180 185 190
 gtg agc agc aac gac aag aaa acc aaa ggc cgg aca ggc tgg cca cag 624
 Val Ser Ser Asn Asp Lys Lys Thr Lys Gly Arg Thr Gly Trp Pro Gln
 195 200 205
 cac gtc tgg gcc ctg gag ctc aag cag 651
 His Val Trp Ala Leu Glu Leu Lys Gln
 210 215

<210> 23

<211> 215

<212> PRT

<213> Homo sapiens

<400> 23

Met Asn Leu Val Gly Ser Tyr Ala His His His His His His His Pro
 1 5 10 15
 His Pro Ala His Pro Met Leu His Glu Pro Phe Leu Phe Gly Pro Ala
 20 25 30

Ser Arg Cys His Gln Glu Arg Pro Tyr Phe Gln Ser Trp Leu Leu Ser
 35 40 45
 Pro Ala Asp Ala Ala Pro Asp Phe Pro Ala Gly Gly Pro Pro Pro Ala
 50 55 60
 Ala Ala Ala Ala Ala Thr Ala Tyr Gly Pro Asp Ala Arg Pro Gly Gln
 65 70 75 80
 Ser Pro Gly Arg Leu Glu Ala Leu Gly Gly Arg Leu Gly Arg Arg Lys
 85 90 95
 Gly Ser Gly Pro Lys Lys Glu Arg Arg Arg Thr Glu Ser Ile Asn Ser
 100 105 110
 Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn Val Pro Ala Asp Thr
 115 120 125
 Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala Thr Ser Tyr Ile Ala
 130 135 140
 Tyr Leu Met Asp Val Leu Ala Lys Asp Ala Gln Ser Gly Asp Pro Glu
 145 150 155 160
 Ala Phe Lys Ala Glu Leu Lys Lys Ala Asp Gly Gly Arg Glu Ser Lys
 165 170 175
 Arg Lys Arg Glu Leu Gln Gln His Glu Gly Phe Pro Pro Ala Leu Gly
 180 185 190
 Pro Val Glu Lys Arg Ile Lys Gly Arg Thr Gly Trp Pro Gln Gln Val
 195 200 205
 Trp Ala Leu Glu Leu Asn Gln
 210

<210> 24

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(648)

<400> 24

atg aac ctc gtg ggc agc tac gca cac cat cac cac cat cac cac ccg 48
 Met Asn Leu Val Gly Ser Tyr Ala His His His His His His Pro
 1 5 10 15
 cac cct gcg cac ccc atg ctc cac gaa ccc ttc ctc ttc ggt ccg gcc 96

His Pro Ala	His Pro Met Leu	His Glu Pro Phe Leu Phe Gly Pro Ala	
20	25	30	
tcg cgc tgt cat cag gaa agg ccc tac ttc cag agc tgg ctg ctg agc			144
Ser Arg Cys His Gln Glu Arg Pro Tyr Phe Gln Ser Trp Leu Leu Ser			
35	40	45	
ccg gct gac gct gcc ccg gac ttc cct gcg ggc ggg ccg ccg ccc gcg			192
Pro Ala Asp Ala Ala Pro Asp Phe Pro Ala Gly Gly Pro Pro Pro Ala			
50	55	60	
gcc gct gca gcc gcc acc gcc tat ggt cct gac gcc agg cct ggg cag			240
Ala Ala Ala Ala Ala Thr Ala Tyr Gly Pro Asp Ala Arg Pro Gly Gln			
65	70	75	80
agc ccc ggg cgg ctg gag gcg ctt ggc ggc cgt ctt ggc cgg cgg aaa			288
Ser Pro Gly Arg Leu Glu Ala Leu Gly Gly Arg Leu Gly Arg Arg Lys			
85	90	95	
ggc tca gga ccc aag aag gag cgg aga cgc act gag agc att aac agc			336
Gly Ser Gly Pro Lys Lys Glu Arg Arg Arg Thr Glu Ser Ile Asn Ser			
100	105	110	
gca ttc gcg gag ttg cgc gag tgc atc ccc aac gtg ccg gcc gac acc			384
Ala Phe Ala Glu Leu Arg Glu Cys Ile Pro Asn Val Pro Ala Asp Thr			
115	120	125	
aag ctc tcc aag atc aag act ctg cgc cta gcc acc agc tac atc gcc			432
Lys Leu Ser Lys Ile Lys Thr Leu Arg Leu Ala Thr Ser Tyr Ile Ala			
130	135	140	
tac ctg atg gac gtg ctg gcc aag gat gca cag tct ggc gat ccc gag			480
Tyr Leu Met Asp Val Leu Ala Lys Asp Ala Gln Ser Gly Asp Pro Glu			
145	150	155	160
gcc ttc aag gct gaa ctc aag aag gcg gat ggc ggc cgt gag agc aag			528
Ala Phe Lys Ala Glu Leu Lys Lys Ala Asp Gly Gly Arg Glu Ser Lys			
165	170	175	
cgg aaa agg gag ctg cag cag cac gaa ggt ttt cct cct gcc ctg ggc			576
Arg Lys Arg Glu Leu Gln Gln His Glu Gly Phe Pro Pro Ala Leu Gly			
180	185	190	
cca gtc gag aag agg att aaa gga cgc acc ggc tgg ccg cag caa gtc			624
Pro Val Glu Lys Arg Ile Lys Gly Arg Thr Gly Trp Pro Gln Gln Val			
195	200	205	
tgg gcg ctg gag tta aac cag			645

Trp Ala Leu Glu Leu Asn Gln

210

215

<210> 25

<211> 411

<212> PRT

<213> Homo sapiens

<400> 25

Met Glu Arg Met Ser Asp Ser Ala Asp Lys Pro Ile Asp Asn Asp Ala

1

5

10

15

Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu

20

25

30

Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu

35

40

45

Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu

50

55

60

Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln

65

70

75

80

Val Leu Ala Arg Arg Lys Ser Arg Asp Phe His Ser Lys Leu Lys Asp

85

90

95

Gln Thr Ala Lys Asp Lys Ala Leu Gln His Met Ala Ala Met Ser Ser

100

105

110

Ala Gln Ile Val Ser Ala Thr Ala Ile His Asn Lys Leu Gly Leu Pro

115

120

125

Gly Ile Pro Arg Pro Thr Phe Pro Gly Ala Pro Gly Phe Trp Pro Gly

130

135

140

Met Ile Gln Thr Gly Gln Pro Gly Ser Ser Gln Asp Val Lys Pro Phe

145

150

155

160

Val Gln Gln Ala Tyr Pro Ile Gln Pro Ala Val Thr Ala Pro Ile Pro

165

170

175

Gly Phe Glu Pro Ala Ser Ala Pro Ala Pro Ser Val Pro Ala Trp Gln

180

185

190

Gly Arg Ser Ile Gly Thr Thr Lys Leu Arg Leu Val Glu Phe Ser Ala

195

200

205

Phe Leu Glu Gln Gln Arg Asp Pro Asp Ser Tyr Asn Lys His Leu Phe

210

215

220

Val His Ile Gly His Ala Asn His Ser Tyr Ser Asp Pro Leu Leu Glu

225 230 235 240
 Ser Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly
 245 250 255
 Gly Leu Lys Glu Leu Phe Gly Lys Gly Pro Gln Asn Ala Phe Phe Leu
 260 265 270
 Val Lys Phe Trp Ala Asp Leu Asn Cys Asn Ile Gln Asp Asp Ala Gly
 275 280 285
 Ala Phe Tyr Gly Val Thr Ser Gln Tyr Glu Ser Ser Glu Asn Met Thr
 290 295 300
 Val Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu
 305 310 315 320
 Lys Val Glu Thr Glu Tyr Ala Arg Phe Glu Asn Gly Arg Phe Val Tyr
 325 330 335
 Arg Ile Asn Arg Ser Pro Met Cys Glu Tyr Met Ile Asn Phe Ile His
 340 345 350
 Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu
 355 360 365
 Asn Phe Thr Ile Leu Leu Val Val Thr Asn Arg Asp Thr Gln Glu Thr
 370 375 380
 Leu Leu Cys Met Ala Cys Val Phe Glu Val Ser Asn Ser Glu His Gly
 385 390 395 400
 Ala Gln His His Ile Tyr Arg Leu Val Lys Asp
 405 410

<210> 26

<211> 1233

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1236)

<400> 26

atg gaa agg atg agt gac tct gca gat aag cca att gac aat gat gca 48
 Met Glu Arg Met Ser Asp Ser Ala Asp Lys Pro Ile Asp Asn Asp Ala
 1 5 10 15
 gaa ggg gtc tgg agc ccc gac atc gag caa agc ttt cag gag gcc ctg 96
 Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu

20	25	30	
gct atc tat cca cca tgt ggg agg agg aaa atc atc tta tca gac gaa			144
Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu			
35	40	45	
ggc aaa atg tat ggt agg aat gaa ttg ata gcc aga tac atc aaa ctc			192
Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu			
50	55	60	
agg aca ggc aag acg agg acc aga aaa cag gtg tct agt cac att cag			240
Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln			
65	70	75	80
ggt ctt gcc aga agg aaa tct cgt gat ttt cat tcc aag cta aag gat			288
Val Leu Ala Arg Arg Lys Ser Arg Asp Phe His Ser Lys Leu Lys Asp			
85	90	95	
cag act gca aag gat aag gcc ctg cag cac atg gcg gcc atg tcc tca			336
Gln Thr Ala Lys Asp Lys Ala Leu Gln His Met Ala Ala Met Ser Ser			
100	105	110	
gcc cag atc gtc tgc gcc act gcc att cat aac aag ctg ggg ctg cct			384
Ala Gln Ile Val Ser Ala Thr Ala Ile His Asn Lys Leu Gly Leu Pro			
115	120	125	
ggg att cca cgc ccg acc ttc cca ggg gcg ccg ggg ttc tgg ccg gga			432
Gly Ile Pro Arg Pro Thr Phe Pro Gly Ala Pro Gly Phe Trp Pro Gly			
130	135	140	
atg att caa aca ggg cag cca gga tcc tca caa gac gtc aag cct ttt			480
Met Ile Gln Thr Gly Gln Pro Gly Ser Ser Gln Asp Val Lys Pro Phe			
145	150	155	160
gtg cag cag gcc tac ccc atc cag cca gcg gtc aca gcc ccc att cca			528
Val Gln Gln Ala Tyr Pro Ile Gln Pro Ala Val Thr Ala Pro Ile Pro			
165	170	175	
ggg ttt gag cct gca tgc gcc cca gct ccc tca gtc cct gcc tgg caa			576
Gly Phe Glu Pro Ala Ser Ala Pro Ala Pro Ser Val Pro Ala Trp Gln			
180	185	190	
ggt cgc tcc att ggc aca acc aag ctt cgc ctg gtg gaa ttt tca gct			624
Gly Arg Ser Ile Gly Thr Thr Lys Leu Arg Leu Val Glu Phe Ser Ala			
195	200	205	
ttt ctc gag cag cag cga gac cca gac tgc tac aac aaa cac ctc ttc			672
Phe Leu Glu Gln Gln Arg Asp Pro Asp Ser Tyr Asn Lys His Leu Phe			

210	215	220	
gtg cac att ggg cat gcc aac cat tct tac agt gac cca ttg ctt gaa			720
Val His Ile Gly His Ala Asn His Ser Tyr Ser Asp Pro Leu Leu Glu			
225	230	235	240
tca gtg gac att cgt cag att tat gac aaa ttt cct gaa aag aaa ggt			768
Ser Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly			
245	250	255	
ggc tta aag gaa ctg ttt gga aag ggc cct caa aat gcc ttc ttc ctc			816
Gly Leu Lys Glu Leu Phe Gly Lys Gly Pro Gln Asn Ala Phe Phe Leu			
260	265	270	
gta aaa ttc tgg gct gat tta aac tgc aat att caa gat gat gct ggg			864
Val Lys Phe Trp Ala Asp Leu Asn Cys Asn Ile Gln Asp Asp Ala Gly			
275	280	285	
gct ttt tat ggt gta acc agt cag tac gag agt tct gaa aat atg aca			912
Ala Phe Tyr Gly Val Thr Ser Gln Tyr Glu Ser Ser Glu Asn Met Thr			
290	295	300	
gtc acc tgt tcc acc aaa gtt tgc tcc ttt ggg aag caa gta gta gaa			960
Val Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu			
305	310	315	320
aaa gta gag acg gag tat gca agg ttt gag aat ggc cga ttt gta tac			1008
Lys Val Glu Thr Glu Tyr Ala Arg Phe Glu Asn Gly Arg Phe Val Tyr			
325	330	335	
cga ata aac cgc tcc cca atg tgt gaa tat atg atc aac ttc atc cac			1056
Arg Ile Asn Arg Ser Pro Met Cys Glu Tyr Met Ile Asn Phe Ile His			
340	345	350	
aag ctc aaa cac tta cca gag aaa tat atg atg aac agt gtt ttg gaa			1104
Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu			
355	360	365	
aac ttc aca att tta ttg gtg gta aca aac agg gat aca caa gaa act			1152
Asn Phe Thr Ile Leu Leu Val Val Thr Asn Arg Asp Thr Gln Glu Thr			
370	375	380	
cta ctc tgc atg gcc tgt gtg ttt gaa gtt tca aat agt gaa cac gga			1200
Leu Leu Cys Met Ala Cys Val Phe Glu Val Ser Asn Ser Glu His Gly			
385	390	395	400
gca caa cat cat att tac agg ctt gta aag gac			1233
Ala Gln His His Ile Tyr Arg Leu Val Lys Asp			

405

410

<210> 27

<211> 427

<212> PRT

<213> Homo sapiens

<400> 27

Ile Thr Ser Asn Glu Trp Ser Ser Pro Thr Ser Pro Glu Gly Ser Thr
 1 5 10 15
 Ala Ser Gly Gly Ser Gln Ala Leu Asp Lys Pro Ile Asp Asn Asp Ala
 20 25 30
 Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu
 35 40 45
 Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu
 50 55 60
 Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu
 65 70 75 80
 Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln
 85 90 95
 Val Leu Ala Arg Arg Lys Ala Arg Glu Ile Gln Ala Lys Leu Lys Asp
 100 105 110
 Gln Ala Ala Lys Asp Lys Ala Leu Gln Ser Met Ala Ala Met Ser Ser
 115 120 125
 Ala Gln Ile Ile Ser Ala Thr Ala Phe His Ser Ser Met Ala Leu Ala
 130 135 140
 Arg Gly Pro Gly Arg Pro Ala Val Ser Gly Phe Trp Gln Gly Ala Leu
 145 150 155 160
 Pro Gly Gln Ala Gly Thr Ser His Asp Val Lys Pro Phe Ser Gln Gln
 165 170 175
 Thr Tyr Ala Val Gln Pro Pro Leu Pro Leu Pro Gly Phe Glu Ser Pro
 180 185 190
 Ala Gly Pro Ala Pro Ser Pro Ser Ala Pro Pro Ala Pro Pro Trp Gln
 195 200 205
 Gly Arg Ser Val Ala Ser Ser Lys Leu Trp Met Leu Glu Phe Ser Ala
 210 215 220
 Phe Leu Glu Gln Gln Gln Asp Pro Asp Thr Tyr Asn Lys His Leu Phe
 225 230 235 240

Val His Ile Gly Gln Ser Ser Pro Ser Tyr Ser Asp Pro Tyr Leu Glu
 245 250 255
 Ala Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly
 260 265 270
 Gly Leu Lys Asp Leu Phe Glu Arg Gly Pro Ser Asn Ala Phe Phe Leu
 275 280 285
 Val Lys Phe Trp Ala Asp Leu Asn Thr Asn Ile Glu Asp Glu Gly Ser
 290 295 300
 Ser Phe Tyr Gly Val Ser Ser Gln Tyr Glu Ser Pro Glu Asn Met Ile
 305 310 315 320
 Ile Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu
 325 330 335
 Lys Val Glu Thr Glu Tyr Ala Arg Tyr Glu Asn Gly His Tyr Ser Tyr
 340 345 350
 Arg Ile His Arg Ser Pro Leu Cys Glu Tyr Met Ile Asn Phe Ile His
 355 360 365
 Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu
 370 375 380
 Asn Phe Thr Ile Leu Gln Val Val Thr Asn Arg Asp Thr Gln Glu Thr
 385 390 395 400
 Leu Leu Cys Ile Ala Tyr Val Phe Glu Val Ser Ala Ser Glu His Gly
 405 410 415
 Ala Gln His His Ile Tyr Arg Leu Val Lys Glu
 420 425

<210> 28

<211> 1281

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1284)

<400> 28

att acc tcc aac gag tgg agc tct ccc acc tcc cct gag ggg agc acc 48
 Ile Thr Ser Asn Glu Trp Ser Ser Pro Thr Ser Pro Glu Gly Ser Thr
 1 5 10 15
 gcc tct ggg ggc agt cag gca ctg gac aag ccc atc gac aat gac gca 96

Ala Ser Gly Gly Ser Gln Ala Leu Asp Lys Pro Ile Asp Asn Asp Ala	
20 25 30	
gag ggc gtg tgg agc ccg gat att gag cag agt ttc cag gag gcc ctc	144
Glu Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu	
35 40 45	
gcc atc tac ccg ccc tgt ggc agg cgc aaa atc atc ctg tgc gac gag	192
Ala Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu	
50 55 60	
ggc aag atg tat ggt cgg aac gag ctg att gcc cgc tac atc aag ctc	240
Gly Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu	
65 70 75 80	
cgg aca ggg aag acc cgc acc agg aag cag gtc tcc agc cac atc cag	288
Arg Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln	
85 90 95	
gtg ctg gct cgt cgc aaa gct cgc gag atc cag gcc aag cta aag gac	336
Val Leu Ala Arg Arg Lys Ala Arg Glu Ile Gln Ala Lys Leu Lys Asp	
100 105 110	
cag gca gct aag gac aag gcc ctg cag agc atg gct gcc atg tgc tct	384
Gln Ala Ala Lys Asp Lys Ala Leu Gln Ser Met Ala Ala Met Ser Ser	
115 120 125	
gca cag atc atc tcc gcc acg gcc ttc cac agt agc atg gcc ctc gcc	432
Ala Gln Ile Ile Ser Ala Thr Ala Phe His Ser Ser Met Ala Leu Ala	
130 135 140	
cgg ggc ccc ggc cgc cca gca gtc tca ggg ttt tgg caa gga gct ttg	480
Arg Gly Pro Gly Arg Pro Ala Val Ser Gly Phe Trp Gln Gly Ala Leu	
145 150 155 160	
cca ggc caa gcc gga acg tcc cat gat gtg aag cct ttc tct cag caa	528
Pro Gly Gln Ala Gly Thr Ser His Asp Val Lys Pro Phe Ser Gln Gln	
165 170 175	
acc tat gct gtc cag cct ccg ctg cct ctg cca ggg ttt gag tct cct	576
Thr Tyr Ala Val Gln Pro Pro Leu Pro Leu Pro Gly Phe Glu Ser Pro	
180 185 190	
gca ggg ccc gcc cca tgc ccc tct gcg ccc ccg gca ccc cca tgg cag	624
Ala Gly Pro Ala Pro Ser Pro Ser Ala Pro Pro Ala Pro Pro Trp Gln	
195 200 205	
ggc cgc agc gtg gcc agc tcc aag ctc tgg atg ttg gag ttc tct gcc	672

Gly Arg Ser Val Ala Ser Ser Lys Leu Trp Met Leu Glu Phe Ser Ala	
210	215 220
ttc ctg gag cag cag cag gac ccg gac acg tac aac aag cac ctg ttc	720
Phe Leu Glu Gln Gln Gln Asp Pro Asp Thr Tyr Asn Lys His Leu Phe	
225	230 235 240
gtg cac att ggc cag tcc agc cca agc tac agc gac ccc tac ctc gaa	768
Val His Ile Gly Gln Ser Ser Pro Ser Tyr Ser Asp Pro Tyr Leu Glu	
245	250 255
gcc gtg gac atc cgc caa atc tat gac aaa ttc ccg gag aaa aag ggt	816
Ala Val Asp Ile Arg Gln Ile Tyr Asp Lys Phe Pro Glu Lys Lys Gly	
260	265 270
gga ctc aag gat ctc ttc gaa cgg gga ccc tcc aat gcc ttt ttt ctt	864
Gly Leu Lys Asp Leu Phe Glu Arg Gly Pro Ser Asn Ala Phe Phe Leu	
275	280 285
gtg aag ttc tgg gca gac ctc aac acc aac atc gag gat gaa ggc agc	912
Val Lys Phe Trp Ala Asp Leu Asn Thr Asn Ile Glu Asp Glu Gly Ser	
290	295 300
tcc ttc tat ggg gtc tcc agc cag tat gag agc ccc gag aac atg atc	960
Ser Phe Tyr Gly Val Ser Ser Gln Tyr Glu Ser Pro Glu Asn Met Ile	
305	310 315 320
atc acc tgc tcc acg aag gtc tgc tct ttc ggc aag cag gtg gtg gag	1008
Ile Thr Cys Ser Thr Lys Val Cys Ser Phe Gly Lys Gln Val Val Glu	
325	330 335
aaa gtt gag aca gag tat gct cgc tat gag aat gga cac tac tct tac	1056
Lys Val Glu Thr Glu Tyr Ala Arg Tyr Glu Asn Gly His Tyr Ser Tyr	
340	345 350
cgc atc cac cgg tcc ccg ctc tgt gag tac atg atc aac ttc atc cac	1104
Arg Ile His Arg Ser Pro Leu Cys Glu Tyr Met Ile Asn Phe Ile His	
355	360 365
aag ctc aag cac ctc cct gag aag tac atg atg aac agc gtg ctg gag	1152
Lys Leu Lys His Leu Pro Glu Lys Tyr Met Met Asn Ser Val Leu Glu	
370	375 380
aac ttc acc atc ctg cag gtg gtc acc aac aga gac aca cag gag acc	1200
Asn Phe Thr Ile Leu Gln Val Val Thr Asn Arg Asp Thr Gln Glu Thr	
385	390 395 400
ttg ctg tgc att gcc tat gtc ttt gag gtg tca gcc agt gag cac ggg	1248

Leu Leu Cys Ile Ala Tyr Val Phe Glu Val Ser Ala Ser Glu His Gly
 405 410 415

gct cag cac cac atc tac agg ctg gtg aaa gaa
 Ala Gln His His Ile Tyr Arg Leu Val Lys Glu
 420 425

1281

<210> 29

<211> 435

<212> PRT

<213> Homo sapiens

<400> 29

Ile Ala Ser Asn Ser Trp Asn Ala Ser Ser Ser Pro Gly Glu Ala Arg
 1 5 10 15

Glu Asp Gly Pro Glu Gly Leu Asp Lys Gly Leu Asp Asn Asp Ala Glu
 20 25 30

Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu Ala
 35 40 45

Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu Gly
 50 55 60

Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu Arg
 65 70 75 80

Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln Val
 85 90 95

Leu Ala Arg Lys Lys Val Arg Glu Tyr Gln Val Gly Ile Lys Ala Met
 100 105 110

Asn Leu Asp Gln Val Ser Lys Asp Lys Ala Leu Gln Ser Met Ala Ser
 115 120 125

Met Ser Ser Ala Gln Ile Val Ser Ala Ser Val Leu Gln Asn Lys Phe
 130 135 140

Ser Pro Pro Ser Pro Leu Pro Gln Ala Val Phe Ser Thr Ser Ser Arg
 145 150 155 160

Phe Trp Ser Ser Pro Pro Leu Leu Gly Gln Gln Pro Gly Pro Ser Gln
 165 170 175

Asp Ile Lys Pro Phe Ala Gln Pro Ala Tyr Pro Ile Gln Pro Pro Leu
 180 185 190

Pro Pro Thr Leu Ser Ser Tyr Glu Pro Leu Ala Pro Leu Pro Ser Ala
 195 200 205

Ala Ala Ser Val Pro Val Trp Gln Asp Arg Thr Ile Ala Ser Ser Arg
 210 215 220
 Leu Arg Leu Leu Glu Tyr Ser Ala Phe Met Glu Val Gln Arg Asp Pro
 225 230 235 240
 Asp Thr Tyr Ser Lys His Leu Phe Val His Ile Gly Gln Thr Asn Pro
 245 250 255
 Ala Phe Ser Asp Pro Pro Leu Glu Ala Val Asp Val Arg Gln Ile Tyr
 260 265 270
 Asp Lys Phe Pro Glu Lys Lys Gly Gly Leu Lys Glu Leu Tyr Glu Lys
 275 280 285
 Gly Pro Pro Asn Ala Phe Phe Leu Val Lys Phe Trp Ala Asp Leu Asn
 290 295 300
 Ser Thr Ile Gln Glu Gly Pro Gly Ala Phe Tyr Gly Val Ser Ser Gln
 305 310 315 320
 Tyr Ser Ser Ala Asp Ser Met Thr Ile Ser Val Ser Thr Lys Val Cys
 325 330 335
 Ser Phe Gly Lys Gln Val Val Glu Lys Val Glu Thr Glu Tyr Ala Arg
 340 345 350
 Leu Glu Asn Gly Arg Phe Val Tyr Arg Ile His Arg Ser Pro Met Cys
 355 360 365
 Glu Tyr Met Ile Asn Phe Ile His Lys Leu Lys His Leu Pro Glu Lys
 370 375 380
 Tyr Met Met Asn Ser Val Leu Glu Asn Phe Thr Ile Leu Gln Val Val
 385 390 395 400
 Thr Ser Arg Asp Ser Gln Glu Thr Leu Leu Val Ile Ala Phe Val Phe
 405 410 415
 Glu Val Ser Thr Ser Glu His Gly Ala Gln His His Val Tyr Lys Leu
 420 425 430

Val Lys Asp

<210> 30

<211> 1305

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1305)

<400> 30

ata gcg tcc aac agc tgg aac gcc agc agc agc ccc ggg gag gcc cgg	48
Ile Ala Ser Asn Ser Trp Asn Ala Ser Ser Ser Pro Gly Glu Ala Arg	
1 5 10 15	
gag gat ggg ccc gag ggc ctg gac aag ggg ctg gac aac gat gcg gag	96
Glu Asp Gly Pro Glu Gly Leu Asp Lys Gly Leu Asp Asn Asp Ala Glu	
20 25 30	
ggc gtg tgg agc ccg gac atc gag cag agc ttc cag gag gcc ctg gcc	144
Gly Val Trp Ser Pro Asp Ile Glu Gln Ser Phe Gln Glu Ala Leu Ala	
35 40 45	
atc tac ccg ccc tgc ggc cgg cgg aag atc atc ctg tca gac gag ggc	192
Ile Tyr Pro Pro Cys Gly Arg Arg Lys Ile Ile Leu Ser Asp Glu Gly	
50 55 60	
aag atg tac ggc cga aat gag ttg att gca cgc tat att aaa ctg agg	240
Lys Met Tyr Gly Arg Asn Glu Leu Ile Ala Arg Tyr Ile Lys Leu Arg	
65 70 75 80	
acg ggg aag act cgg acg aga aaa cag gtg tcc agc cac ata cag gtt	288
Thr Gly Lys Thr Arg Thr Arg Lys Gln Val Ser Ser His Ile Gln Val	
85 90 95	
cta gct cgg aag aag gtg cgg gag tac cag gtt ggc atc aag gcc atg	336
Leu Ala Arg Lys Lys Val Arg Glu Tyr Gln Val Gly Ile Lys Ala Met	
100 105 110	
aac ctg gac cag gtc tcc aag gac aaa gcc ctt cag agc atg gcg tcc	384
Asn Leu Asp Gln Val Ser Lys Asp Lys Ala Leu Gln Ser Met Ala Ser	
115 120 125	
atg tcc tct gcc cag atc gtc tct gcc agt gtc ctg cag aac aag ttc	432
Met Ser Ser Ala Gln Ile Val Ser Ala Ser Val Leu Gln Asn Lys Phe	
130 135 140	
agc cca cct tcc cct ctg ccc cag gcc gtc ttc tcc act tcc tgc cgg	480
Ser Pro Pro Ser Pro Leu Pro Gln Ala Val Phe Ser Thr Ser Ser Arg	
145 150 155 160	
ttc tgg agc agc ccc cct etc ctg gga cag cag cct gga ccc tct cag	528
Phe Trp Ser Ser Pro Pro Leu Leu Gly Gln Gln Pro Gly Pro Ser Gln	
165 170 175	
gac atc aag ccc ttt gca cag cca gcc tac ccc atc cag ccg ccc ctg	576
Asp Ile Lys Pro Phe Ala Gln Pro Ala Tyr Pro Ile Gln Pro Pro Leu	

180	185	190	
ccg ccg acg ctc agc agt tat gag ccc ctg gcc ccg ctc ccc tca gct			624
Pro Pro Thr Leu Ser Ser Tyr Glu Pro Leu Ala Pro Leu Pro Ser Ala			
195	200	205	
gct gcc tct gtg cct gtg tgg cag gac cgt acc att gcc tcc tcc cgg			672
Ala Ala Ser Val Pro Val Trp Gln Asp Arg Thr Ile Ala Ser Ser Arg			
210	215	220	
ctg cgg ctc ctg gag tat tca gcc ttc atg gag gtg cag cga gac cct			720
Leu Arg Leu Leu Glu Tyr Ser Ala Phe Met Glu Val Gln Arg Asp Pro			
225	230	235	240
gac acg tac agc aaa cac ctg ttt gtg cac atc gcc cag acg aac ccc			768
Asp Thr Tyr Ser Lys His Leu Phe Val His Ile Gly Gln Thr Asn Pro			
245	250	255	
gcc ttc tca gac cca ccc ctg gag gca gta gat gtg cgc cag atc tat			816
Ala Phe Ser Asp Pro Pro Leu Glu Ala Val Asp Val Arg Gln Ile Tyr			
260	265	270	
gac aaa ttc ccc gag aaa aag gga gga ttg aag gag ctc tat gag aag			864
Asp Lys Phe Pro Glu Lys Lys Gly Gly Leu Lys Glu Leu Tyr Glu Lys			
275	280	285	
ggg ccc cct aat gcc ttc ttc ctt gtc aag ttc tgg gcc gac ctc aac			912
Gly Pro Pro Asn Ala Phe Phe Leu Val Lys Phe Trp Ala Asp Leu Asn			
290	295	300	
agc acc atc cag gag gcc ccg gga gcc ttc tat ggg gtc agc tct cag			960
Ser Thr Ile Gln Glu Gly Pro Gly Ala Phe Tyr Gly Val Ser Ser Gln			
305	310	315	320
tac agc tct gct gat agc atg acc atc agc gtc tcc acc aag gtg tgc			1008
Tyr Ser Ser Ala Asp Ser Met Thr Ile Ser Val Ser Thr Lys Val Cys			
325	330	335	
tcc ttt gcc aaa cag gtg gta gag aag gtg gag act gag tat gcc agg			1056
Ser Phe Gly Lys Gln Val Val Glu Lys Val Glu Thr Glu Tyr Ala Arg			
340	345	350	
ctg gag aac ggg cgc ttt gtg tac cgt atc cac cgc tgc ccc atg tgc			1104
Leu Glu Asn Gly Arg Phe Val Tyr Arg Ile His Arg Ser Pro Met Cys			
355	360	365	
gag tac atg atc aac ttc atc cac aag ctg aag cac ctg ccc gag aag			1152
Glu Tyr Met Ile Asn Phe Ile His Lys Leu Lys His Leu Pro Glu Lys			

370 375 380
 tac atg atg aac agc gtg ctg gag aac ttc acc atc ctg cag gtg gtc 1200
 Tyr Met Met Asn Ser Val Leu Glu Asn Phe Thr Ile Leu Gln Val Val
 385 390 395 400
 acg agc cgg gac tcc cag gag acc ttg ctt gtc att gct ttt gtc ttc 1248
 Thr Ser Arg Asp Ser Gln Glu Thr Leu Leu Val Ile Ala Phe Val Phe
 405 410 415
 gaa gtc tcc acc agt gag cac ggg gcc cag cac cat gtc tac aag ctc 1296
 Glu Val Ser Thr Ser Glu His Gly Ala Gln His His Val Tyr Lys Leu
 420 425 430
 gtc aaa gac 1305
 Val Lys Asp
 435
 <210> 31
 <211> 1132
 <212> PRT
 <213> Homo sapiens
 <400> 31
 Met Pro Arg Ala Pro Arg Cys Arg Ala Val Arg Ser Leu Leu Arg Ser
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 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
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 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140

Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430

Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720

Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
 835 840 845
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
 930 935 940
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005

Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
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<210> 32

<211> 3396

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(3399)

<400> 32

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 cac tac cgc gag gtg ctg ccg ctg gcc acg ttc gtg cgg cgc ctg ggg 96
 His Tyr Arg Glu Val Leu Pro Leu Ala Thr Phe Val Arg Arg Leu Gly
 20 25 30
 ccc cag gcc tgg cgg ctg gtg cag cgc ggg gac ccg gcg gct ttc cgc 144
 Pro Gln Gly Trp Arg Leu Val Gln Arg Gly Asp Pro Ala Ala Phe Arg
 35 40 45
 gcg ctg gtg gcc cag tgc ctg gtg tgc gtg ccc tgg gac gca cgg ccg 192
 Ala Leu Val Ala Gln Cys Leu Val Cys Val Pro Trp Asp Ala Arg Pro
 50 55 60

ccc ccc gcc gcc ccc tcc ttc cgc cag gtg tcc tgc ctg aag gag ctg 240
 Pro Pro Ala Ala Pro Ser Phe Arg Gln Val Ser Cys Leu Lys Glu Leu
 65 70 75 80
 gtg gcc cga gtg ctg cag agg ctg tgc gag cgc ggc gcg aag aac gtg 288
 Val Ala Arg Val Leu Gln Arg Leu Cys Glu Arg Gly Ala Lys Asn Val
 85 90 95
 ctg gcc ttc ggc ttc gcg ctg ctg gac ggg gcc cgc ggg ggc ccc ccc 336
 Leu Ala Phe Gly Phe Ala Leu Leu Asp Gly Ala Arg Gly Gly Pro Pro
 100 105 110
 gag gcc ttc acc acc agc gtg cgc agc tac ctg ccc aac acg gtg acc 384
 Glu Ala Phe Thr Thr Ser Val Arg Ser Tyr Leu Pro Asn Thr Val Thr
 115 120 125
 gac gca ctg cgg ggg agc ggg gcg tgg ggg ctg ctg ctg cgc cgc gtg 432
 Asp Ala Leu Arg Gly Ser Gly Ala Trp Gly Leu Leu Leu Arg Arg Val
 130 135 140
 ggc gac gac gtg ctg gtt cac ctg ctg gca cgc tgc gcg ctc ttt gtg 480
 Gly Asp Asp Val Leu Val His Leu Leu Ala Arg Cys Ala Leu Phe Val
 145 150 155 160
 ctg gtg gct ccc agc tgc gcc tac cag gtg tgc ggg ccg ccg ctg tac 528
 Leu Val Ala Pro Ser Cys Ala Tyr Gln Val Cys Gly Pro Pro Leu Tyr
 165 170 175
 cag ctc ggc gct gcc act cag gcc cgg ccc ccg cca cac gct agt gga 576
 Gln Leu Gly Ala Ala Thr Gln Ala Arg Pro Pro Pro His Ala Ser Gly
 180 185 190
 ccc cga agg cgt ctg gga tgc gaa cgg gcc tgg aac cat agc gtc agg 624
 Pro Arg Arg Arg Leu Gly Cys Glu Arg Ala Trp Asn His Ser Val Arg
 195 200 205
 gag gcc ggg gtc ccc ctg ggc ctg cca gcc ccg ggt gcg agg agg cgc 672
 Glu Ala Gly Val Pro Leu Gly Leu Pro Ala Pro Gly Ala Arg Arg Arg
 210 215 220
 ggg ggc agt gcc agc cga agt ctg ccg ttg ccc aag agg ccc agg cgt 720
 Gly Gly Ser Ala Ser Arg Ser Leu Pro Leu Pro Lys Arg Pro Arg Arg
 225 230 235 240
 ggc gct gcc cct gag ccg gag cgg acg ccc gtt ggg cag ggg tcc tgg 768
 Gly Ala Ala Pro Glu Pro Glu Arg Thr Pro Val Gly Gln Gly Ser Trp
 245 250 255

gcc cac ccg ggc agg acg cgt gga ccg agt gac cgt ggt ttc tgt gtg 816
 Ala His Pro Gly Arg Thr Arg Gly Pro Ser Asp Arg Gly Phe Cys Val
 260 265 270
 gtg tca cct gcc aga ccc gcc gaa gaa gcc acc tct ttg gag ggt gcg 864
 Val Ser Pro Ala Arg Pro Ala Glu Glu Ala Thr Ser Leu Glu Gly Ala
 275 280 285
 ctc tct ggc acg cgc cac tcc cac cca tcc gtg ggc cgc cag cac cac 912
 Leu Ser Gly Thr Arg His Ser His Pro Ser Val Gly Arg Gln His His
 290 295 300
 gcg ggc ccc cca tcc aca tgc cgg cca cca cgt ccc tgg gac acg cct 960
 Ala Gly Pro Pro Ser Thr Ser Arg Pro Pro Arg Pro Trp Asp Thr Pro
 305 310 315 320
 tgt ccc ccg gtg tac gcc gag acc aag cac ttc ctc tac tcc tca ggc 1008
 Cys Pro Pro Val Tyr Ala Glu Thr Lys His Phe Leu Tyr Ser Ser Gly
 325 330 335
 gac aag gag cag ctg cgg ccc tcc ttc cta ctc agc tct ctg agg ccc 1056
 Asp Lys Glu Gln Leu Arg Pro Ser Phe Leu Leu Ser Ser Leu Arg Pro
 340 345 350
 agc ctg act ggc gct cgg agg ctc gtg gag acc atc ttt ctg ggt tcc 1104
 Ser Leu Thr Gly Ala Arg Arg Leu Val Glu Thr Ile Phe Leu Gly Ser
 355 360 365
 agg ccc tgg atg cca ggg act ccc cgc agg ttg ccc cgc ctg ccc cag 1152
 Arg Pro Trp Met Pro Gly Thr Pro Arg Arg Leu Pro Arg Leu Pro Gln
 370 375 380
 cgc tac tgg caa atg cgg ccc ctg ttt ctg gag ctg ctt ggg aac cac 1200
 Arg Tyr Trp Gln Met Arg Pro Leu Phe Leu Glu Leu Leu Gly Asn His
 385 390 395 400
 gcg cag tgc ccc tac ggg gtg ctc ctc aag acg cac tgc ccg ctg cga 1248
 Ala Gln Cys Pro Tyr Gly Val Leu Leu Lys Thr His Cys Pro Leu Arg
 405 410 415
 get gcg gtc acc cca gca gcc ggt gtc tgt gcc cgg gag aag ccc cag 1296
 Ala Ala Val Thr Pro Ala Ala Gly Val Cys Ala Arg Glu Lys Pro Gln
 420 425 430
 ggc tct gtg gcg gcc ccc gag gag gag gac aca gac ccc cgt cgc ctg 1344
 Gly Ser Val Ala Ala Pro Glu Glu Glu Asp Thr Asp Pro Arg Arg Leu
 435 440 445

gtg cag ctg ctc cgc cag cac agc agc ccc tgg cag gtg tac ggc ttc 1392
 Val Gln Leu Leu Arg Gln His Ser Ser Pro Trp Gln Val Tyr Gly Phe
 450 455 460
 gtg cgg gcc tgc ctg cgc cgg ctg gtg ccc cca ggc ctc tgg ggc tcc 1440
 Val Arg Ala Cys Leu Arg Arg Leu Val Pro Pro Gly Leu Trp Gly Ser
 465 470 475 480
 agg cac aac gaa cgc cgc ttc ctc agg aac acc aag aag ttc atc tcc 1488
 Arg His Asn Glu Arg Arg Phe Leu Arg Asn Thr Lys Lys Phe Ile Ser
 485 490 495
 ctg ggg aag cat gcc aag ctc tgc ctg cag gag ctg acg tgg aag atg 1536
 Leu Gly Lys His Ala Lys Leu Ser Leu Gln Glu Leu Thr Trp Lys Met
 500 505 510
 agc gtg cgg gac tgc gct tgg ctg cgc agg agc cca ggg gtt ggc tgt 1584
 Ser Val Arg Asp Cys Ala Trp Leu Arg Arg Ser Pro Gly Val Gly Cys
 515 520 525
 gtt ccg gcc gca gag cac cgt ctg cgt gag gag atc ctg gcc aag ttc 1632
 Val Pro Ala Ala Glu His Arg Leu Arg Glu Glu Ile Leu Ala Lys Phe
 530 535 540
 ctg cac tgg ctg atg agt gtg tac gtc gtc gag ctg ctc agg tct ttc 1680
 Leu His Trp Leu Met Ser Val Tyr Val Val Glu Leu Leu Arg Ser Phe
 545 550 555 560
 ttt tat gtc acg gag acc acg ttt caa aag aac agg ctc ttt ttc tac 1728
 Phe Tyr Val Thr Glu Thr Thr Phe Gln Lys Asn Arg Leu Phe Phe Tyr
 565 570 575
 cgg aag agt gtc tgg agc aag ttg caa agc att gga atc aga cag cac 1776
 Arg Lys Ser Val Trp Ser Lys Leu Gln Ser Ile Gly Ile Arg Gln His
 580 585 590
 ttg aag agg gtg cag ctg cgg gag ctg tgc gaa gca gag gtc agg cag 1824
 Leu Lys Arg Val Gln Leu Arg Glu Leu Ser Glu Ala Glu Val Arg Gln
 595 600 605
 cat cgg gaa gcc agg ccc gcc ctg ctg acg tcc aga ctc cgc ttc atc 1872
 His Arg Glu Ala Arg Pro Ala Leu Leu Thr Ser Arg Leu Arg Phe Ile
 610 615 620
 ccc aag cct gac ggg ctg cgg cgg att gtg aac atg gac tac gtc gtg 1920
 Pro Lys Pro Asp Gly Leu Arg Pro Ile Val Asn Met Asp Tyr Val Val
 625 630 635 640

gga gcc aga acg ttc cgc aga gaa aag agg gcc gag cgt ctc acc tcg 1968
 Gly Ala Arg Thr Phe Arg Arg Glu Lys Arg Ala Glu Arg Leu Thr Ser
 645 650 655
 agg gtg aag gca ctg ttc agc gtg ctc aac tac gag cgg gcg cgg cgc 2016
 Arg Val Lys Ala Leu Phe Ser Val Leu Asn Tyr Glu Arg Ala Arg Arg
 660 665 670
 ccc ggc ctc ctg ggc gcc tct gtg ctg ggc ctg gac gat atc cac agg 2064
 Pro Gly Leu Leu Gly Ala Ser Val Leu Gly Leu Asp Asp Ile His Arg
 675 680 685
 gcc tgg cgc acc ttc gtg ctg cgt gtg cgg gcc cag gac ccg ccg cct 2112
 Ala Trp Arg Thr Phe Val Leu Arg Val Arg Ala Gln Asp Pro Pro Pro
 690 695 700
 gag ctg tac ttt gtc aag gtg gat gtg acg ggc gcg tac gac acc atc 2160
 Glu Leu Tyr Phe Val Lys Val Asp Val Thr Gly Ala Tyr Asp Thr Ile
 705 710 715 720
 ccc cag gac agg ctc acg gag gtc atc gcc agc atc atc aaa ccc cag 2208
 Pro Gln Asp Arg Leu Thr Glu Val Ile Ala Ser Ile Ile Lys Pro Gln
 725 730 735
 aac acg tac tgc gtg cgt cgg tat gcc gtg gtc cag aag gcc gcc cat 2256
 Asn Thr Tyr Cys Val Arg Arg Tyr Ala Val Val Gln Lys Ala Ala His
 740 745 750
 ggg cac gtc cgc aag gcc ttc aag agc cac gtc tct acc ttg aca gac 2304
 Gly His Val Arg Lys Ala Phe Lys Ser His Val Ser Thr Leu Thr Asp
 755 760 765
 ctc cag ccg tac atg cga cag ttc gtg gct cac ctg cag gag acc agc 2352
 Leu Gln Pro Tyr Met Arg Gln Phe Val Ala His Leu Gln Glu Thr Ser
 770 775 780
 ccg ctg agg gat gcc gtc gtc atc gag cag agc tcc tcc ctg aat gag 2400
 Pro Leu Arg Asp Ala Val Val Ile Glu Gln Ser Ser Ser Leu Asn Glu
 785 790 795 800
 gcc agc agt ggc ctc ttc gac gtc ttc cta cgc ttc atg tgc cac cac 2448
 Ala Ser Ser Gly Leu Phe Asp Val Phe Leu Arg Phe Met Cys His His
 805 810 815
 gcc gtg cgc atc agg ggc aag tcc tac gtc cag tgc cag ggg atc ccg 2496
 Ala Val Arg Ile Arg Gly Lys Ser Tyr Val Gln Cys Gln Gly Ile Pro
 820 825 830

cag ggc tcc atc ctc tcc acg ctg ctc tgc agc ctg tgc tac ggc gac 2544
 Gln Gly Ser Ile Leu Ser Thr Leu Leu Cys Ser Leu Cys Tyr Gly Asp
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 atg gag aac aag ctg ttt gcg ggg att cgg cgg gac ggg ctg ctc ctg 2592
 Met Glu Asn Lys Leu Phe Ala Gly Ile Arg Arg Asp Gly Leu Leu Leu
 850 855 860
 cgt ttg gtg gat gat ttc ttg ttg gtg aca cct cac ctc acc cac gcg 2640
 Arg Leu Val Asp Asp Phe Leu Leu Val Thr Pro His Leu Thr His Ala
 865 870 875 880
 aaa acc ttc ctg agg acc ctg gtc cga ggt gtc cct gag tat ggc tgc 2688
 Lys Thr Phe Leu Arg Thr Leu Val Arg Gly Val Pro Glu Tyr Gly Cys
 885 890 895
 gtg gtg aac ttg cgg aag aca gtg gtg aac ttc cct gta gaa gac gag 2736
 Val Val Asn Leu Arg Lys Thr Val Val Asn Phe Pro Val Glu Asp Glu
 900 905 910
 gcc ctg ggt ggc acg gct ttt gtt cag atg ccg gcc cac ggc cta ttc 2784
 Ala Leu Gly Gly Thr Ala Phe Val Gln Met Pro Ala His Gly Leu Phe
 915 920 925
 ccc tgg tgc ggc ctg ctg ctg gat acc cgg acc ctg gag gtg cag agc 2832
 Pro Trp Cys Gly Leu Leu Leu Asp Thr Arg Thr Leu Glu Val Gln Ser
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 gac tac tcc agc tat gcc cgg acc tcc atc aga gcc agt ctc acc ttc 2880
 Asp Tyr Ser Ser Tyr Ala Arg Thr Ser Ile Arg Ala Ser Leu Thr Phe
 945 950 955 960
 aac cgc ggc ttc aag gct ggg agg aac atg cgt cgc aaa ctc ttt ggg 2928
 Asn Arg Gly Phe Lys Ala Gly Arg Asn Met Arg Arg Lys Leu Phe Gly
 965 970 975
 gtc ttg cgg ctg aag tgt cac agc ctg ttt ctg gat ttg cag gtg aac 2976
 Val Leu Arg Leu Lys Cys His Ser Leu Phe Leu Asp Leu Gln Val Asn
 980 985 990
 agc ctc cag acg gtg tgc acc aac atc tac aag atc ctc ctg ctg cag 3024
 Ser Leu Gln Thr Val Cys Thr Asn Ile Tyr Lys Ile Leu Leu Leu Gln
 995 1000 1005
 gcg tac agg ttt cac gca tgt gtg ctg cag ctc cca ttt cat cag caa 3072
 Ala Tyr Arg Phe His Ala Cys Val Leu Gln Leu Pro Phe His Gln Gln
 1010 1015 1020

gtt tgg aag aac ccc aca ttt ttc ctg cgc gtc atc tct gac acg gcc 3120
 Val Trp Lys Asn Pro Thr Phe Phe Leu Arg Val Ile Ser Asp Thr Ala
 1025 1030 1035 1040
 tcc ctc tgc tac tcc atc ctg aaa gcc aag aac gca ggg atg tgc ctg 3168
 Ser Leu Cys Tyr Ser Ile Leu Lys Ala Lys Asn Ala Gly Met Ser Leu
 1045 1050 1055
 ggg gcc aag ggc gcc gcc ggc cct ctg ccc tcc gag gcc gtg cag tgg 3216
 Gly Ala Lys Gly Ala Ala Gly Pro Leu Pro Ser Glu Ala Val Gln Trp
 1060 1065 1070
 ctg tgc cac caa gca ttc ctg ctc aag ctg act cga cac cgt gtc acc 3264
 Leu Cys His Gln Ala Phe Leu Leu Lys Leu Thr Arg His Arg Val Thr
 1075 1080 1085
 tac gtg cca ctc ctg ggg tca ctc agg aca gcc cag acg cag ctg agt 3312
 Tyr Val Pro Leu Leu Gly Ser Leu Arg Thr Ala Gln Thr Gln Leu Ser
 1090 1095 1100
 cgg aag ctc ccg ggg acg acg ctg act gcc ctg gag gcc gca gcc aac 3360
 Arg Lys Leu Pro Gly Thr Thr Leu Thr Ala Leu Glu Ala Ala Ala Asn
 1105 1110 1115 1120
 ccg gca ctg ccc tca gac ttc aag acc atc ctg gac 3396
 Pro Ala Leu Pro Ser Asp Phe Lys Thr Ile Leu Asp
 1125 1130

<210> 33

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer sequence

<400> 33

ttggttcca ggccataatt g 21

<210> 34

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 34

20

aagagggcag atctatcgga

<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 35

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atggatctcc tgaagtgct

<210> 36

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 36

20

aagagggcag atctatcgga

<210> 37

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 37

23

ggaagagtga gcggccatca agg

<210> 38

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 38

22

ctgctggaga ggttattcct cg

<210> 39

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 39

24

gccaacacca acctgtccaa gttc

<210> 40

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 40

24

tgcaaaggct ccaggtctga gggc

<210> 41

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 41

19

ctctctctcc tcaggacaa

<210> 42

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 42

22

tggagcaaaa cagaatggct gg

<210> 43

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 43

24

ctgagatgtc tctctctctc ttag

<210> 44

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 44

20

acaatgactg atgagagatg

<210> 45

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 45

18

cagacctgaa ggagacct

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 46

18

gtcagcgtaa acagttgc

<210> 47

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 47

20

gccaaagaagc ggatagaagg

<210> 48

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 48

20

ctgtggttca gggctcagtc

<210> 49

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 49

20

cagtggagct ggacaaagcc

<210> 50

<211> 20

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 50

tagcgacggt tctggaacca

20

<210> 51

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 51

ctgtcatctc actatgggca

20

<210> 52

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 52

ccaagtccga gcaggaattt

20

<210> 53

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 53

aagacgtcaa gccctttgtg

20

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 54

20

aaaggagcac actttggtgg

<210> 55

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 55

20

agcaagaata cgatgccatc

<210> 56

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223>Description of Artificial Sequence: artificially
synthesized primer sequence

<400> 56

20

gaaggggtgg tggtacggtc

<210> 57

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 57

20

tgggaatggc tatgtcagtg

<210> 58

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 58

ctggtaatct gtgtttagg

20

<210> 59

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 59

caagggcctc tccaaacttg

20

<210> 60

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: artificially synthesized primer
sequence

<400> 60

gccccagaga cagcattcca

20

<210> 61

<211> 268

<212> PRT

<213> Homo sapiens

<400> 61

Met Ala Gln Pro Leu Cys Pro Pro Leu Ser Glu Ser Trp Met Leu Ser

1

5

10

15

Ala Ala Trp Gly Pro Thr Arg Arg Pro Pro Pro Ser Asp Lys Asp Cys

20

25

30

Gly Arg Ser Leu Val Ser Ser Pro Asp Ser Trp Gly Ser Thr Pro Ala

35

40

45

Asp Ser Pro Val Ala Ser Pro Ala Arg Pro Gly Thr Leu Arg Asp Pro
 50 55 60

Arg Ala Pro Ser Val Gly Arg Arg Gly Ala Arg Ser Ser Arg Leu Gly
 65 70 75 80

Ser Gly Gln Arg Gln Ser Ala Ser Glu Arg Glu Lys Leu Arg Met Arg
 85 90 95

Thr Leu Ala Arg Ala Leu His Glu Leu Arg Arg Phe Leu Pro Pro Ser
 100 105 110

Val Ala Pro Ala Gly Gln Ser Leu Thr Lys Ile Glu Thr Leu Arg Leu
 115 120 125

Ala Ile Arg Tyr Ile Gly His Leu Ser Ala Val Leu Gly Leu Ser Glu
 130 135 140

Glu Ser Leu Gln Arg Arg Cys Arg Gln Arg Gly Asp Ala Gly Ser Pro
 145 150 155 160

Arg Gly Cys Pro Leu Cys Pro Asp Asp Cys Pro Ala Gln Met Gln Thr
 165 170 175

Arg Thr Gln Ala Glu Gly Gln Gly Gln Gly Arg Gly Leu Gly Leu Val
 180 185 190

Ser Ala Val Arg Ala Gly Ala Ser Trp Gly Ser Pro Pro Ala Cys Pro
 195 200 205

Gly Ala Arg Ala Ala Pro Glu Pro Arg Asp Pro Pro Ala Leu Phe Ala
 210 215 220

Glu Ala Ala Cys Pro Glu Gly Gln Ala Met Glu Pro Ser Pro Pro Ser
 225 230 235 240

Pro Leu Leu Pro Gly Asp Val Leu Ala Leu Leu Glu Thr Trp Met Pro
 245 250 255

Leu Ser Pro Leu Glu Trp Leu Pro Glu Glu Pro Lys
 260 265

<210> 62

<211> 804

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(807)

<400> 62

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gcg gcc tgg ggc cca act cgg ccg ccg ccc tcc gac aag gac tgc 96
 Ala Ala Trp Gly Pro Thr Arg Arg Pro Pro Pro Ser Asp Lys Asp Cys
 20 25 30

ggc cgc tcc ctc gtc tgc tcc cca gac tca tgg ggc agc acc cca gcc 144
 Gly Arg Ser Leu Val Ser Ser Pro Asp Ser Trp Gly Ser Thr Pro Ala
 35 40 45

gac agc ccc gtg gcg agc ccc gcg ccg cca ggc acc ctc cgg gac ccc 192
 Asp Ser Pro Val Ala Ser Pro Ala Arg Pro Gly Thr Leu Arg Asp Pro
 50 55 60

cgc gcc ccc tcc gta ggt agg cgc ggc gcg cgc agc agc cgc ctg ggc 240
 Arg Ala Pro Ser Val Gly Arg Arg Gly Ala Arg Ser Ser Arg Leu Gly
 65 70 75 80

agc ggg cag agg cag agc gcc agt gag ccg gag aaa ctg cgc atg cgc 288
 Ser Gly Gln Arg Gln Ser Ala Ser Glu Arg Glu Lys Leu Arg Met Arg
 85 90 95

acg ctg gcc cgc gcc ctg cac gag ctg cgc cgc ttt cta ccg ccg tcc 336
 Thr Leu Ala Arg Ala Leu His Glu Leu Arg Arg Phe Leu Pro Pro Ser
 100 105 110

gtg gcg ccc gcg ggc cag agc ctg acc aag atc gag acg ctg cgc ctg 384
 Val Ala Pro Ala Gly Gln Ser Leu Thr Lys Ile Glu Thr Leu Arg Leu
 115 120 125

gct atc cgc tat atc ggc cac ctg tcg gcc gtg cta ggc ctc agc gag 432
 Ala Ile Arg Tyr Ile Gly His Leu Ser Ala Val Leu Gly Leu Ser Glu
 130 135 140

gag agt ctc cag cgc cgg tgc cgg cag cgc ggt gac gcg ggg tcc cct 480
 Glu Ser Leu Gln Arg Arg Cys Arg Gln Arg Gly Asp Ala Gly Ser Pro
 145 150 155 160

cgg ggc tgc ccg ctg tgc ccc gac gac tgc ccc gcg cag atg cag aca 528
 Arg Gly Cys Pro Leu Cys Pro Asp Asp Cys Pro Ala Gln Met Gln Thr
 165 170 175

cgg acg cag gct gag ggg cag ggg cag ggg cgc ggg ctg ggc ctg gta 576
 Arg Thr Gln Ala Glu Gly Gln Gly Gln Gly Arg Gly Leu Gly Leu Val
 180 185 190

tcc gcc gtc cgc gcc ggg gcg tcc tgg gga tcc ccg cct gcc tgc ccc 624
 Ser Ala Val Arg Ala Gly Ala Ser Trp Gly Ser Pro Pro Ala Cys Pro
 195 200 205

gga gcc cga gct gca ccc gag ccg cgc gac ccg cct gcg ctg ttc gcc 672
 Gly Ala Arg Ala Ala Pro Glu Pro Arg Asp Pro Pro Ala Leu Phe Ala
 210 215 220

gag gcg gcg tgc cct gaa ggg cag gcg atg gag cca agc cca ccg tcc 720
 Glu Ala Ala Cys Pro Glu Gly Gln Ala Met Glu Pro Ser Pro Pro Ser
 225 230 235 240

ccg ctc ctt ccg ggc gac gtg ctg gct ctg ttg gag acc tgg atg ccc 768
 Pro Leu Leu Pro Gly Asp Val Leu Ala Leu Leu Glu Thr Trp Met Pro
 245 250 255

ctc tcg cct ctg gag tgg ctg cct gag gag ccc aag 804
 Leu Ser Pro Leu Glu Trp Leu Pro Glu Glu Pro Lys
 260 265

<210> 63

<211> 215

<212> PRT

<213> Homo sapiens

<400> 63

Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
 1 5 10 15

Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
 20 25 30

Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
 35 40 45

Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
 50 55 60

Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
 65 70 75 80

Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg
 85 90 95

Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys
 100 105 110

Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val
 115 120 125

Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala
 130 135 140

Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg
 145 150 155 160

Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys
 165 170 175

Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu
 180 185 190

Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
 195 200 205

Thr Trp Ala Pro Glu Pro Arg
 210

<210> 64

<211> 645

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(648)

<400> 64

atg ggc agc ccc cgc tcc gcg ctg agc tgc ctg ctg ttg cac ttg ctg 48
 Met Gly Ser Pro Arg Ser Ala Leu Ser Cys Leu Leu Leu His Leu Leu
 1 5 10 15

gtc ctc tgc ctc caa gcc cag gta act gtt cag tcc tca cct aat ttt 96
 Val Leu Cys Leu Gln Ala Gln Val Thr Val Gln Ser Ser Pro Asn Phe
 20 25 30

aca cag cat gtg agg gag cag agc ctg gtg acg gat cag ctc agc cgc 144

Thr Gln His Val Arg Glu Gln Ser Leu Val Thr Asp Gln Leu Ser Arg
35 40 45

cgc ctc atc cgg acc tac caa ctc tac agc cgc acc agc ggg aag cac 192
Arg Leu Ile Arg Thr Tyr Gln Leu Tyr Ser Arg Thr Ser Gly Lys His
50 55 60

gtg cag gtc ctg gcc aac aag cgc atc aac gcc atg gca gag gac ggc 240
Val Gln Val Leu Ala Asn Lys Arg Ile Asn Ala Met Ala Glu Asp Gly
65 70 75 80

gac ccc ttc gca aag ctc atc gtg gag acg gac acc ttt gga agc aga 288
Asp Pro Phe Ala Lys Leu Ile Val Glu Thr Asp Thr Phe Gly Ser Arg
85 90 95

gtt cga gtc cga gga gcc gag acg ggc ctc tac atc tgc atg aac aag 336
Val Arg Val Arg Gly Ala Glu Thr Gly Leu Tyr Ile Cys Met Asn Lys
100 105 110

aag ggg aag ctg atc gcc aag agc aac ggc aaa ggc aag gac tgc gtc 384
Lys Gly Lys Leu Ile Ala Lys Ser Asn Gly Lys Gly Lys Asp Cys Val
115 120 125

ttc acg gag att gtg ctg gag aac aac tac aca gcg ctg cag aat gcc 432
Phe Thr Glu Ile Val Leu Glu Asn Asn Tyr Thr Ala Leu Gln Asn Ala
130 135 140

aag tac gag ggc tgg tac atg gcc ttc acc cgc aag ggc cgg ccc cgc 480
Lys Tyr Glu Gly Trp Tyr Met Ala Phe Thr Arg Lys Gly Arg Pro Arg
145 150 155 160

aag ggc tcc aag acg cgg cag cac cag cgt gag gtc cac ttc atg aag 528
Lys Gly Ser Lys Thr Arg Gln His Gln Arg Glu Val His Phe Met Lys
165 170 175

cgg ctg ccc cgg ggc cac cac acc acc gag cag agc ctg cgc ttc gag 576

Arg Leu Pro Arg Gly His His Thr Thr Glu Gln Ser Leu Arg Phe Glu
 180 185 190

ttc ctc aac tac ccg ccc ttc acg cgc agc ctg cgc ggc agc cag agg 624
 Phe Leu Asn Tyr Pro Pro Phe Thr Arg Ser Leu Arg Gly Ser Gln Arg
 195 200 205

act tgg gcc ccg gaa ccc cga 645
 Thr Trp Ala Pro Glu Pro Arg
 210 215

<210> 65

<211> 212

<212> PRT

<213> Homo sapiens

<400> 65

Met Asp Tyr Leu Leu Met Ile Phe Ser Leu Leu Phe Val Ala Cys Gln
 1 5 10 15

Gly Ala Pro Glu Thr Ala Val Leu Gly Ala Glu Leu Ser Ala Val Gly
 20 25 30

Glu Asn Gly Gly Glu Lys Pro Thr Pro Ser Pro Pro Trp Arg Leu Arg
 35 40 45

Arg Ser Lys Arg Cys Ser Cys Ser Ser Leu Met Asp Lys Glu Cys Val
 50 55 60

Tyr Phe Cys His Leu Asp Ile Ile Trp Val Asn Thr Pro Glu His Val
 65 70 75 80

Val Pro Tyr Gly Leu Gly Ser Pro Arg Ser Lys Arg Ala Leu Glu Asn
 85 90 95

Leu Leu Pro Thr Lys Ala Thr Asp Arg Glu Asn Arg Cys Gln Cys Ala
 100 105 110

Ser Gln Lys Asp Lys Lys Cys Trp Asn Phe Cys Gln Ala Gly Lys Glu
 115 120 125

Leu Arg Ala Glu Asp Ile Met Glu Lys Asp Trp Asn Asn His Lys Lys
 130 135 140

Gly Lys Asp Cys Ser Lys Leu Gly Lys Lys Cys Ile Tyr Gln Gln Leu
 145 150 155 160

Val Arg Gly Arg Lys Ile Arg Arg Ser Ser Glu Glu His Leu Arg Gln
 165 170 175

Thr Arg Ser Glu Thr Met Arg Asn Ser Val Lys Ser Ser Phe His Asp
 180 185 190

Pro Lys Leu Lys Gly Lys Pro Ser Arg Glu Arg Tyr Val Thr His Asn
 195 200 205

Arg Ala His Trp
 210

<210> 66

<211> 636

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(639)

<400> 66

atg gat tat ttg ctc atg att ttc tct ctg ctg ttt gtg gct tgc caa 48
 Met Asp Tyr Leu Leu Met Ile Phe Ser Leu Leu Phe Val Ala Cys Gln
 1 5 10 15

gga gct cca gaa aca gca gtc tta ggc gct gag ctc agc gcg gtg ggt 96
 Gly Ala Pro Glu Thr Ala Val Leu Gly Ala Glu Leu Ser Ala Val Gly
 20 25 30

gag aac ggc ggg gag aaa ccc act ccc agt cca ccc tgg cgg ctc cgc 144
 Glu Asn Gly Gly Glu Lys Pro Thr Pro Ser Pro Pro Trp Arg Leu Arg

35

40

45

cgg tcc aag cgc tgc tcc tgc tgc tcc ctg atg gat aaa gag tgt gtc 192
 Arg Ser Lys Arg Cys Ser Cys Ser Ser Leu Met Asp Lys Glu Cys Val

50

55

60

tac ttc tgc cac ctg gac atc att tgg gtc aac act ccc gag cac gtt 240
 Tyr Phe Cys His Leu Asp Ile Ile Trp Val Asn Thr Pro Glu His Val

65

70

75

80

gtt ccg tat gga ctt gga agc cct agg tcc aag aga gcc ttg gag aat 288
 Val Pro Tyr Gly Leu Gly Ser Pro Arg Ser Lys Arg Ala Leu Glu Asn

85

90

95

tta ctt ccc aca aag gca aca gac cgt gag aat aga tgc caa tgt gct 336
 Leu Leu Pro Thr Lys Ala Thr Asp Arg Glu Asn Arg Cys Gln Cys Ala

100

105

110

agc caa aaa gac aag aag tgc tgg aat ttt tgc caa gca gga aaa gaa 384
 Ser Gln Lys Asp Lys Lys Cys Trp Asn Phe Cys Gln Ala Gly Lys Glu

115

120

125

ctc agg gct gaa gac att atg gag aaa gac tgg aat aat cat aag aaa 432
 Leu Arg Ala Glu Asp Ile Met Glu Lys Asp Trp Asn Asn His Lys Lys

130

135

140

gga aaa gac tgt tcc aag ctt ggg aaa aag tgt att tat cag cag tta 480
 Gly Lys Asp Cys Ser Lys Leu Gly Lys Lys Cys Ile Tyr Gln Gln Leu

145

150

155

160

gtg aga gga aga aaa atc aga aga agt tca gag gaa cac cta aga caa 528
 Val Arg Gly Arg Lys Ile Arg Arg Ser Ser Glu Glu His Leu Arg Gln

165

170

175

acc agg tgc gag acc atg aga aac agc gtc aaa tca tct ttt cat gat 576
 Thr Arg Ser Glu Thr Met Arg Asn Ser Val Lys Ser Ser Phe His Asp
 180 185 190

ccc aag ctg aaa ggc aag ccc tcc aga gag cgt tat gtg acc cac aac 624
 Pro Lys Leu Lys Gly Lys Pro Ser Arg Glu Arg Tyr Val Thr His Asn
 195 200 205

ega gca cat tgg 636
 Arg Ala His Trp
 210

<210> 67

<211> 143

<212> PRT

<213> Homo sapiens

<400> 67

Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
 1 5 10 15

Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly
 20 25 30

Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
 35 40 45

Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
 50 55 60

Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
 65 70 75 80

Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly
 85 90 95

Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr
 100 105 110

Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro
 115 120 125

Lys Thr Lys Ala Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
 130 135 140

<210> 68

<211> 429

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(432)

<400> 68

atg cag cac cga ggc ttc ctc ctc ctc acc ctc ctc gcc ctg ctg gcg 48
 Met Gln His Arg Gly Phe Leu Leu Leu Thr Leu Leu Ala Leu Leu Ala
 1 5 10 15

ctc acc tcc gcg gtc gcc aaa aag aaa gat aag gtg aag aag ggc ggc 96
 Leu Thr Ser Ala Val Ala Lys Lys Lys Asp Lys Val Lys Lys Gly Gly
 20 25 30

ccg ggg agc gag tgc gct gag tgg gcc tgg ggg ccc tgc acc ccc agc 144
 Pro Gly Ser Glu Cys Ala Glu Trp Ala Trp Gly Pro Cys Thr Pro Ser
 35 40 45

agc aag gat tgc ggc gtg ggt ttc cgc gag ggc acc tgc ggg gcc cag 192
 Ser Lys Asp Cys Gly Val Gly Phe Arg Glu Gly Thr Cys Gly Ala Gln
 50 55 60

acc cag cgc atc cgg tgc agg gtg ccc tgc aac tgg aag aag gag ttt 240
 Thr Gln Arg Ile Arg Cys Arg Val Pro Cys Asn Trp Lys Lys Glu Phe
 65 70 75 80

gga gcc gac tgc aag tac aag ttt gag aac tgg ggt gcg tgt gat ggg 288
 Gly Ala Asp Cys Lys Tyr Lys Phe Glu Asn Trp Gly Ala Cys Asp Gly

85

90

95

ggc aca ggc acc aaa gtc cgc caa ggc acc ctg aag aag gcg cgc tac 336
 Gly Thr Gly Thr Lys Val Arg Gln Gly Thr Leu Lys Lys Ala Arg Tyr
 100 105 110

aat gct cag tgc cag gag acc atc cgc gtc acc aag ccc tgc acc ccc 384
 Asn Ala Gln Cys Gln Glu Thr Ile Arg Val Thr Lys Pro Cys Thr Pro
 115 120 125

aag acc aaa gca aag gcc aaa gcc aag aaa ggg aag gga aag gac 429
 Lys Thr Lys Ala Lys Ala Lys Lys Gly Lys Gly Lys Asp
 130 135 140

<210> 69

<211> 408

<212> PRT

<213> Homo sapiens

<400> 69

Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val
 1 5 10 15

Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys
 20 25 30

Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly
 35 40 45

Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met
 50 55 60

Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro
 65 70 75 80

Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu
 85 90 95

Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser
100 105 110

Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn
115 120 125

Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu
130 135 140

Ser Ser Ile Pro Glu Asn Glu Ala Ile Ser Ser Ala Glu Leu Arg Leu
145 150 155 160

Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His
165 170 175

Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro
180 185 190

Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn
195 200 205

Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp
210 215 220

Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His
225 230 235 240

Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg
245 250 255

Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu
260 265 270

Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg
275 280 285

Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
 290 295 300

Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
 305 310 315 320

Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
 325 330 335

Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
 340 345 350

Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
 355 360 365

Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
 370 375 380

Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
 385 390 395 400

Val Val Glu Gly Cys Gly Cys Arg
 405

<210> 70

<211> 1224

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<223> (1)..(1227)

<400> 70

atg att cct ggt aac cga atg ctg atg gtc gtt tta tta tgc caa gtc 48

Met Ile Pro Gly Asn Arg Met Leu Met Val Val Leu Leu Cys Gln Val

1

5

10

15

ctg cta gga ggc gcg agc cat gct agt ttg ata cct gag acg ggg aag 96

Leu Leu Gly Gly Ala Ser His Ala Ser Leu Ile Pro Glu Thr Gly Lys
 20 25 30

aaa aaa gtc gcc gag att cag ggc cac gcg gga gga cgc cgc tca ggg 144
 Lys Lys Val Ala Glu Ile Gln Gly His Ala Gly Gly Arg Arg Ser Gly
 35 40 45

cag agc cat gag ctc ctg egg gac ttc gag gcg aca ctt ctg cag atg 192
 Gln Ser His Glu Leu Leu Arg Asp Phe Glu Ala Thr Leu Leu Gln Met
 50 55 60

ttt ggg ctg cgc cgc cgc cgc cag cct agc aag agt gcc gtc att ccg 240
 Phe Gly Leu Arg Arg Arg Pro Gln Pro Ser Lys Ser Ala Val Ile Pro
 65 70 75 80

gac tac atg cgg gat ctt tac cgg ctt cag tct ggg gag gag gag gaa 288
 Asp Tyr Met Arg Asp Leu Tyr Arg Leu Gln Ser Gly Glu Glu Glu Glu
 85 90 95

gag cag atc cac agc act ggt ctt gag tat cct gag cgc ccg gcc agc 336
 Glu Gln Ile His Ser Thr Gly Leu Glu Tyr Pro Glu Arg Pro Ala Ser
 100 105 110

cgg gcc aac acc gtg agg agc ttc cac cac gaa gaa cat ctg gag aac 384
 Arg Ala Asn Thr Val Arg Ser Phe His His Glu Glu His Leu Glu Asn
 115 120 125

atc cca ggg acc agt gaa aac tct get ttt cgt ttc ctc ttt aac ctc 432
 Ile Pro Gly Thr Ser Glu Asn Ser Ala Phe Arg Phe Leu Phe Asn Leu
 130 135 140

agc agc atc cct gag aac gag gcg atc tcc tct gca gag ctt cgg ctc 480
 Ser Ser Ile Pro Glu Asn Glu Ala Ile Ser Ser Ala Glu Leu Arg Leu
 145 150 155 160

ttc cgg gag cag gtg gac cag ggc cct gat tgg gaa agg ggc ttc cac 528

Phe Arg Glu Gln Val Asp Gln Gly Pro Asp Trp Glu Arg Gly Phe His
 165 170 175

cgt ata aac att tat gag gtt atg aag ccc cca gca gaa gtg gtg cct 576
 Arg Ile Asn Ile Tyr Glu Val Met Lys Pro Pro Ala Glu Val Val Pro
 180 185 190

ggg cac ctc atc aca cga cta ctg gac acg aga ctg gtc cac cac aat 624
 Gly His Leu Ile Thr Arg Leu Leu Asp Thr Arg Leu Val His His Asn
 195 200 205

gtg aca cgg tgg gaa act ttt gat gtg age cct gcg gtc ctt cgc tgg 672
 Val Thr Arg Trp Glu Thr Phe Asp Val Ser Pro Ala Val Leu Arg Trp
 210 215 220

acc cgg gag aag cag cca aac tat ggg cta gcc att gag gtg act cac 720
 Thr Arg Glu Lys Gln Pro Asn Tyr Gly Leu Ala Ile Glu Val Thr His
 225 230 235 240

ctc cat cag act cgg acc cac cag ggc cag cat gtc agg att agc cga 768
 Leu His Gln Thr Arg Thr His Gln Gly Gln His Val Arg Ile Ser Arg
 245 250 255

tgc tta cct caa ggg agt ggg aat tgg gcc cag ctc cgg ccc ctc ctg 816
 Ser Leu Pro Gln Gly Ser Gly Asn Trp Ala Gln Leu Arg Pro Leu Leu
 260 265 270

gtc acc ttt ggc cat gat ggc cgg ggc cat gcc ttg acc cga cgc cgg 864
 Val Thr Phe Gly His Asp Gly Arg Gly His Ala Leu Thr Arg Arg Arg
 275 280 285

agg gcc aag cgt agc cct aag cat cac tca cag cgg gcc agg aag aag 912
 Arg Ala Lys Arg Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys
 290 295 300

aat aag aac tgc cgg cgc cac tgc ctc tat gtg gac ttc agc gat gtg 960

Asn Lys Asn Cys Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val
 305 310 315 320

ggc tgg aat gac tgg att gtg gcc cca cca ggc tac cag gcc ttc tac 1008
 Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr
 325 330 335

tgc cat ggg gac tgc ccc ttt cca ctg gct gac cac ctc aac tca acc 1056
 Cys His Gly Asp Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr
 340 345 350

aac cat gcc att gtg cag acc ctg gtc aat tct gtc aat tcc agt atc 1104
 Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile
 355 360 365

ccc aaa gcc tgt tgt gtg ccc act gaa ctg agt gcc atc tcc atg ctg 1152
 Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu
 370 375 380

tac ctg gat gag tat gat aag gtg gta ctg aaa aat tat cag gag atg 1200
 Tyr Leu Asp Glu Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met
 385 390 395 400

gta gta gag gga tgt ggg tgc cgc 1224
 Val Val Glu Gly Cys Gly Cys Arg
 405

<210> 71

<211> 24

<212> DNA

<213> Artificial Sequence

<400> 71

gcccgcgctc caactgctct gatg

24

<210> 72

<211> 24

<212> DNA

<213> Artificial Sequence

<400> 72

24

tgcctacggt ggtgcgccct ctgc

<210> 73

<211> 22

<212> DNA

<213> Artificial Sequence

<400> 73

22

gaagcgcaac agggccatca cg

<210> 74

<211> 22

<212> DNA

<213> Artificial Sequence

<400> 74

22

ccacgtcacg caggtcccgt tc

<210> 75

<211> 22

<212> DNA

<213> Artificial Sequence

<400> 75

22

gatcctgttc tctgcctctg ga

<210> 76

<211> 22

<212> DNA

<213> Artificial Sequence

<400> 76

22

tcateccactt tgtccaccg ag

<210> 77

<211> 21

<212> DNA

<213> Artificial Sequence

<400> 77

ttcctcgtct tggccttttg g

21

<210> 78

<211> 21

<212> DNA

<213> Artificial Sequence

<400> 78

gctggatctt cgtaggctcc g

21

<210> 79

<211> 19

<212> DNA

<213> Artificial Sequence

<400> 79

ggcaagctga ccctgaagt

19

<210> 80

<211> 19

<212> DNA

<213> Artificial Sequence

<400> 80

gggtgctcag gtagtggtt

19